

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 01:27:42 ; Search time 3689 Seconds

(without alignments)
9947.394 Million cell updates/sec

Title: US-09-811-094-3

Perfect score: 897
Sequence: 1 atgacgagcagcagccatctc.....agctcaagaaggtgactctaa 897

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: gb_hcg:*
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40: em_hlgo_mus:*
41: em_hlgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	100.0	897	6 AX134720	AX134720 Sequence
2	897	100.0	897	6 AX301848	AX301848 Sequence
3	897	100.0	1399	9 BC031912	BC031912 Homo sapi
4	895.4	99.8	1193	9 BC008935	BC008935 Homo sapi
5	895.4	99.8	1308	9 BC007295	BC007295 Homo sapi
6	895.4	99.8	1344	9 AY007135	AY007135 Homo sapi
7	895.4	99.8	1366	9 BC007850	BC007850 Homo sapi
8	895.4	99.8	1455	9 BC014775	BC014775 Homo sapi
9	895.4	99.8	1466	9 BC008737	BC008737 Homo sapi
10	774.4	86.3	1349	4 BOV121RANS	BOV121RANS
11	771.2	86.0	1116	6 AX337175	AX337175 Sequence
12	771.2	86.0	1116	6 AX409449	AX409449 Sequence
13	771.2	86.0	1116	9 HDMTICA	HDMTICA
14	758.4	84.5	291762	2 AC125887	AC125887 Rattus no
15	704.6	78.6	169550	5 AL354854	AL354854 Human DNA
16	618.6	69.0	1266	5 AF506216	AF506216 Dario rer
17	609	67.9	932	4 AB009386	AB009386 Oryctolag
18	605.8	67.5	1194	4 BOV11FRANS	M24102 Bovine ADP/
19	597.8	66.6	1010	5 AB088686	AB088686 Gallus ga
20	596.2	66.5	1196	6 AX401651	AX401651 Sequence
21	596.2	66.5	1196	10 RATANT1	D12770 Rattus norv
22	596.2	66.5	1215	10 RATANT2	D12771 Rattus norv
23	594.6	66.3	897	6 AX134719	AX134719 Sequence
24	594.6	66.3	897	6 AX301847	AX301847 Sequence
25	594.6	66.3	1146	4 AB065433	AB065433 Bos tauru
26	594.6	66.3	1228	9 HDMATPC	J02683 Human ADP/A
27	593	66.1	897	10 MMT10404	U10404 Mus musculu
28	593	66.1	1070	10 BC026925	BC026925 Mus muscu
29	593	66.1	1142	10 BC003791	BC003791 Mus muscu
30	593	66.1	1236	10 BC004570	BC004570 Mus muscu
31	593	66.1	1244	10 MM027316	U27316 Mus musculu
32	593	66.1	1273	10 MM027315	U27315 Mus musculu
33	593	66.1	1280	10 MMTANTAP	X70847 M.musculus
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38	580.2	64.7	231319	10 AC122916	AC122916 Mus muscu
39	572	63.8	246444	2 AC130772	AC130772 Rattus no
40	572	63.8	258818	2 AC135265	AC135265 Rattus no
41	569.8	63.5	238007	2 AC112888	AC112888 Rattus no
42	569.8	63.5	309949	2 AC111573	AC111573 Rattus no
43	567.4	63.3	242738	2 AC110340	AC110340 Rattus no
44	564.2	62.9	894	6 AX134718	AX134718 Sequence
45	564.2	62.9	894	6 AX301846	AX301846 Sequence

ALIGNMENTS

RESULT 1
AX134720 897 bp DNA linear PAT 29-MAY-2001
LOCUS AX134720
DEFINITION Sequence 3 from Patent WO0132876.
ACCESSION AX134720
VERSION AX134720.1 GI:14271237
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Murphy,A.N., Clevenger,W., Wiley,S.E., Andrew,A.Y., Frigert,L.G.,
Veliciedl,G. and Davis,R.E.
TITLE Compositions and methods for determining interactions of

Pred. No. is the number of results predicted by chance to have a

mitochondrial components, and for identifying agents that alter such interactions
Patent: WO 0132876-A 3 10-MAY-2001;
JOURNAL

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Best Local Similarity 100.0%; Pred. No. 6.8e-132;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 841 GGCATGGGGGGGCGCCCTTCGTGCTGGTCTGTACGACGAGCTCAAGAGGTGATCTAA 897

RESULT 2					
AX301848	AX301848	897 bp	DNA	linear	PAT 30-NOV-2001
LOCUS	Sequence 3 from Patent WO0185944.				
DEFINITION	AX301848				
ACCESSION	AX301848				
VERSION	AX301848.1	GI:17382905			

SOURCE

REFERENCE

AUTHORS ANDERSON, R.L., DEVEREAUX, C.E., HENNING, M., HAZEN, J.M., SZABO, T.R., GHOSH, S.S., MOOS, W.H., PELI, Y. and CERRITO, A.K.
TITLE Production of adenine nucleotide translocator (ant), novel ant ligands and screening assays therefor
JOURNAL Patent: WO 0165944-A 3 15-NOV-2001.

FEATURES

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Oy	121	GCCAGCAAGCAGATCGCGCGCAGACAAGCATACAGAGGCATCTGAGCTGCATTTGCCG	180
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Db 878 GGCATGGGGGCGCCCTTCTGCTGCTCTTACAGCAGCTCAAGAAGTGATCTAA 934
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BC008935
LOCUS Homo sapiens, similar to solute carrier family 25 (mitochondrial
DEFINITION carrier; adenine nucleotide translocator), member 5, clone MGC:2387
IMAGE:2824067, mRNA, complete cds.
ACCESSION BC008935 GI:14286273
VERSION MGC.
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Rachel Dikchoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettelman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov
Series: IMAL Plate: 2 Row: n Column: 21
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BC007295
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DEFINITION adenine nucleotide translocator), member 6, mRNA (CDNA clone
MGC:15671 IMAGE:3349670), complete cds.
ACCESSION BC007295 GI:13938330
VERSION MGC.
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS
Strausberg, R.L., Feligold, E.A., Grouse, L.H., Derge, J.G.,
1 (bases 1 to 1308)
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buecaw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McKean, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M.,
Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smallus, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL
MEDLINE
22388257
PUBMED
12477932
REFERENCE
AUTHORS
2 (bases 1 to 1308)
Strausberg, R.
Direct Submission
Submitted (01-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
REMARK
COMMENT
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzyzanski, Kela Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carlie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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1 ATGACGAACAGGCGCATCTCTCGCAAAAGATTCTTGCCGAGGACATCGCGCGGC 60
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353 GGGGGGTGGAGCAAGACAGCGATCTGGAGTACTTGGCGGCAACCTGGCGTCCGCG 412
361 GGTGGCGCGCGCGACCTCTCTCTCTCTGTTACCCCGTGGATTTGGCAAGACCCG 420
413 GGTGGCGCGCGCGACCTCTCTCTCTCTGTTACCCCGTGGATTTGGCGAACC 472
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713 ACCGCGCGTGGCGCGTGGTCTCTACCCCTTGACACAGTGGCGGCGCATGATGATG 772
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841 GCGATGGGGGGCGCTTCTGCTGCTGTCTGTACGAGAGAGCTCAAGAAAGTGTATCTAA 897

REMARK

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shcherbko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Diehl, N.L., Guan, X., Gupta, J., Ho, S.L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCluskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantford, S., Thomas, P.J.,
Thompson, E.E., Touchman, J.W., Tsurguev, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 20 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BASE COUNT 287 a 419 c 409 g 251 t

Query Match 99.8%; Score 895.4; DB 9; Length 1366;
Best Local Similarity 99.9%; Pred. No. 1.1e-131;
Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ATCTCCAAAGCGCGTGGCTCGATCGAGCGGGGTCAACTGCTGTCGACGTCAGCAC 120
DB 161 ATCTCCAAAGCGCGTGGCTCGATCGAGCGGGGTCAACTGCTGTCGACGTCAGCAC 220
QY 121 GCGAGCAAGCAGATCGCGCGCGCAAGAGTACAAAGGCGATGCGTGCATTCGCCG 180
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QY 301 GGGGGGTGGACACAGCAGCAGTCTTGGAGGTACTTGGCGGCAACTGGCTCCGGC 360
DB 401 GGGGGGTGGACACAGCAGCAGTCTTGGAGGTACTTGGCGGCAACTGGCTCCGGC 460
QY 361 GGTGGCGCGCGCGACCTCCCTTGCCTTGTGTAACCCGCTGATTTTCCGAACCCGC 420
DB 461 GGTGGCGCGCGCGACCTCCCTTGCCTTGTGTAACCCGCTGATTTTCCGAACCCGC 520
QY 421 CTGGCAGCGAGCTGGGAAAGTACAGCAGCGGAGTTCGAGCGCTGGAGACTGC 480
DB 521 CTGGCAGCGAGCTGGGAAAGTACAGCAGCGGAGTTCGAGCGCTGGAGACTGC 580
QY 481 CTGGTGAAGATACCAAGTCCGACAGCATCGGGGCTTACAGAGGCTTCAGTGTCC 540
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DB 701 ATGCTCCCGACCGCCCAAGACACGACATCTGTGTAGCTGATGATCGCGACCGTG 760
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DB 941 GGCATGGGGGGCGCTTGTGCTGTGCTGTGACAGCATCAAGAGGTGATCTAA 997

RESULT 8
BC014775
LOCUS
DEFINITION
Homo sapiens, similar to solute carrier family 25 (mitochondrial
carrier; adenine nucleotide translocator), member 5, clone
MGC:17525 IMAGE:3458777, mRNA, complete cds.

ACCESSION
BC014775
VERSION
BC014775.1 GI:15928607
SOURCE
MGC.
ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 1455)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.
Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HQSC
Web site: <http://www.hqsc.bcm.tmc.edu/cdna/>
Contact: villalobdc@bcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Huliyil, S., Lu, X., Garcia, A.M., Hollaway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRK Plate: 19 Row: P Column: 11.
Location/Qualifiers

FEATURES

source

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member 5"
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BASE COUNT

308 a 440 c 431 g 276 t

Query Match 99.8%; Score 895.4; DB 9; Length 1455;
Best Local Similarity 99.9%; Pred. No. 1.1e-131;
Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 ATGACGACAGGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCGCC 60
93 ATGACGACAGGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCGCC 152
61 ATCTCCAGAGCGCGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCG 120
153 ATCTCCAGAGCGCGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCG 212
121 GCGACGACAGGCGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCG 180
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181 ATCTCCAGAGCGCGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCG 240
273 ATCTCCAGAGCGCGCGCATCTCTGCGCAAGACTTCTGCGCGAGGATCGCGCGCG 332
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333 TACTTCCCGCACTCAACCTTCAACTGCGCTTCAAGGATTAAGTACAGAGACTTCTCC 392
301 GGGGGCGGTGACAGACACGAGTTCGAGGATTCCTGCGCGCAACCTGCGCGCGCG 360
393 GGGGGCGGTGACAGACACGAGTTCGAGGATTCCTGCGCGCAACCTGCGCGCGCG 452
361 GGTGCGGGCGGGGCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
453 GGTGCGGGCGGGGCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
421 CTGGACAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCGAGGCGTGGAGACTGC 480
513 CTGGACAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCGAGGCGTGGAGACTGC 572
481 CTGGTGAAGATCCACCAAGTCGAGCGGATTCGCGGGCGCTTACAGAGGCTTCACTGCTCC 540
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661 AGGCGCGTGGCGGCGGTGTGTCTTACCCCTTTCGACACGCGTGGCGGCGGCGGATGATG 720
753 AGGCGCGTGGCGGCGGTGTGTCTTACCCCTTTCGACACGCGTGGCGGCGGCGGATGATG 812
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RESULT 9
LOCUS BC008737
DEFINITION Homo sapiens, similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MGC:3042 IMAGE:3342722, mRNA, complete cds.
ACCESSION BC008737
VERSION BC008737.1 GI:14250566
KEYWORDS MGC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1466)
AUTHORS Kammalya, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgap@ncl.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: <http://www.nisc.nih.gov/>
nisc.mgc@ncl.nih.gov
Shevchenko, Y., Wetherby, R.D., Beckstrom, Sternberg, S.M., Benjamini, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastaglio, C., Mastrilian, S.D., McLoake, J.C., McDowell, J., Pearson, R., Snyder, B., Staniford, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsugeon, C., Vogt, D.L., Walker, M.A., Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRK Plate: 5 Row: o Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

source

Location/Qualifiers

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/db_xref="taxon:9606"

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CDS

BASE COUNT

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ORIGIN

Query Match

Best Local Similarity 99.8%; Score 895.4; DB 9; Length 1466;

Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGAGGGAACAGCCATCTCTCCGCAAGACCTTGGCCGAGGCAATCCGCCGCC 60

89 ATGAGGGAACAGCCATCTCTCCGCAAGACCTTGGCCGAGGCAATCCGCCGCC 148

61 ATCTCCAGACGGCGCTGCTCGATCGAGGGGTCACCTGCTGTCGAGGTCAGCAG 120

149 ATCTCCAGACGGCGCTGCTCGATCGAGGGGTCACCTGCTGTCGAGGTCAGCAG 208

121 GCCAGCAGACAGATCGCCCGCAGACAGATCAAGAGGATGATGATGATGATGAT 180

209 GCCAGCAGACAGATCGCCCGCAGACAGATCAAGAGGATGATGATGATGATGAT 268

181 ATCCCCAAGAGGAGGCGCTGCTCTCTGAGAGGGGCAACCTTCCCAAGTCATGCG 240

269 ATCCCCAAGAGGAGGCGCTGCTCTCTGAGAGGGGCAACCTTCCCAAGTCATGCG 328

241 TACTTCCCACTCAAGCCCTCAACTCGCTTCAAGAGATAGTCAAGAGATCTCTCG 300

329 TACTTCCCACTCAAGCCCTCAACTCGCTTCAAGAGATAGTCAAGAGATCTCTCG 388

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361 GGTGGCGCGCGGCGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

449 GGTGGCGCGCGGCGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508

421 CTGGCAGGCGAGCTGGGGAAGTCAAGCAGACAGCGGATTCGAGAGCTGGAGACTGC 480

509 CTGGCAGGCGAGCTGGGGAAGTCAAGCAGACAGCGGATTCGAGAGCTGGAGACTGC 568

481 CTGTGAAGATCAACCAAGTCCGACGATCCGGGGCTTACCAAGGCTTCAAGTCTCC 540

569 CTGTGAAGATCAACCAAGTCCGACGATCCGGGGCTTACCAAGGCTTCAAGTCTCC 628

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689 ATGCTCCCGACCCCAAGAACGACGATCGTGTGATGATGATGATGATGATGATG 748

661 ACGGCCGTGGCGCGCTGCTGCTTACCCCTTCAGACAGCGTCCGGCGGCATGATGATG 720

749 ACGGCCGTGGCGCGCTGCTGCTTACCCCTTCAGACAGCGTCCGGCGGCATGATGATG 808

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RESULT 10

BOVT27TRANS

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

1 (bases 1 to 1349)

Powell,S.J., Medd,S.M., Runswick,M.J. and Walker,J.E.

Two bovine genes for mitochondrial Adp/ATP translocase expressed differences in various tissues

Biochemistry 28 (2), 866-873 (1989)

89228093

2540808

COMMENT

On Aug 13, 1994 this sequence version replaced gi:341114.

Original source text: Bos taurus cDNA to mRNA.

LOCATION/QUALIFIERS

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CDS

BASE COUNT

242 a 447 c 409 g 251 t

ORIGIN

Query Match

Best Local Similarity 86.3%; Score 774.4; DB 4; Length 1349;

Matches 820; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

1 ATGAGGGAACAGCCATCTCTCCGCAAGACCTTGGCCGAGGCAATCCGCCGCC 60

64 ATGAGGGAACAGCCATCTCTCCGCAAGACCTTGGCCGAGGCAATCCGCCGCC 123

61 ATCTCCAGACGGCGCTGCTCGATCGAGGGGTCACCTGCTGTCGAGTCCAGCAC 120

124 ATCTCCAGACGGCGCTGCTCGATCGAGGGGTCACCTGCTGTCGAGTCCAGCAC 183

121 GCCAGCAGACAGATCGCCCGCAGACAGTCAAGAGGATGATGATGATGATGATG 180

Db	184	GCAGAACAGAGATCGGGCCGACAAAGAGTACAAAGGGGACTGTGGACTGATCGTGGCT	243
Oy	181	ATCCCCAAGAGAGAGGGGGTGTCGTCCCTTCGTGGAGGGGGCAACCTTGGCAACGTCAATTCGC	240
Db	244	ATCCCAAGAGAGAGGGGGCTGTCGTCTTCCTTCGGCGGGGCACCTGGCCAACTGATCCG	303
Oy	241	TACTTCCCACTCAACCCCTCAACTGTGGCCCTCAAGATAACTACAGCAATCTTCTCG	300
Db	304	TATTTTCCCAAGACAGCGCTCAACTTGCCTTTCAAAAGACATACAGCAATATCTTCTCG	363
Oy	301	GGGGGGCTGGACACACACACAGTCTTGGAGGTACTTTGGCGGCACCTGGCCCTCGGC	360
Db	364	GGGGGGCTGGACAAAGGGCAACAGTCTTGGAGGTACTTTGGCGGCACCTGGCCCTCGGC	423
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Db	424	GGGGGGGGCCGAGCCACTTTCCTGTGTGTGTGTACCCGCTGGATTTTGGCAGAACCCG	483
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Db	484	CTGGCGGGCCACCTGGGGCAAGTGGGGCAGTGTAGCCGAGTTTCAGGGGCTGGAGATGTG	543
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Oy	601	ATGCTCCGCCACCCCAAGAAACAGGACATCGTGTGATAGTGTATGGCGCAAGCCGG	660
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Oy	661	ACGGCCGTGGCGGGGGTGTCGTACCCCTGTGACACAGGTGGCGGGCGCATGATGATG	720
Db	724	ACGGCCGTGGCGGGGGTGTCGTACCCCTGTGACACAGGTGGCGGGCGCATGATGATG	783
Oy	721	CAGTCGGGGGGCAAAAGCACTGACATCTGATACACGGGCACCGTGTGATGGAGGAAG	780
Db	784	CAGTCGGGGGGCAAAAGCACTGACATCTGATACACGGGCACCGTGTGATGGAGGAAG	843
Oy	781	ATCTTCAGAGATAGGGGGGCAAGGCGCTTCTCAAGGGTGGGTGGTCCACGTCCTGGG	840
Db	844	ATCTTCAGAGATAGGGGGGCAAGGCGCTTCTCAAGGGTGGGTGGTCCACGTCCTGGG	903
Oy	841	GGCATGGGGGGGCGCTTCTGTGCTGTCTGTACGACAGACTCAAGAGATGATCTTA	896
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LOCUS	AX337175	1116 bp	DNA
DEFINITION	Sequence 7684 from Patent WO0194629.		
ACCESSION	AX337175		
VERSION	AX337175.1		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G., Horriagan, S., Soppet, D.R. and Weaver, Z.		
TITLE	Cancer gene determination and therapeutic screening using signature gene sets		
JOURNAL	Patent: WO 0194629-A 7684 13-DEC-2001; Avalon Pharmaceuticals (US)		
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Best Local Similarity	99.28;	Pred. No. 4.3e-112;			
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Db	1	GTGAGGTTCAGCAGCGCCAGCAGCAGATCCGCCCGCAGACAGCAGTACACAGGCGATCGTG	60		
OY	166	GACTCATTTGTTCGCATCCCAAGAGCAGGGCGTGTCTCTTCTTGAGGGGCAACTT	225		
Db	61	GACTCATTTGTTCGCATCCCAAGAGAGAGGGCGTGTCTCTTCTTGAGGGGCAACTT	120		
OY	226	GCCAAAGCTATTCGCTACTTCCCACTCAAGCCCTCAACTTTCGCTTCAAGAGTAAGTAC	285		
Db	121	GCCAAAGCTATTCGCTACTTCCCACTCAAGCCCTCAACTTTCGCTTCAAGAGTAAGTAC	180		
OY	286	AAGCAGATCTTCCTGGGGGGCGTGGACACAGCAGCAGTCTTGAGAGTACTTTCGGGGC	345		
Db	181	AAGCAGATCTTCCTGGGGGGCGTGGACAGCAGCAGCAGTCTTGAGAGTACTTTCGGGGC	237		
OY	346	AACCTGGCTTCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	405		
Db	238	AACCTGGCTTCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	297		
OY	406	TTTGGCAGAAACCG	465		
Db	298	TTTGGCAGAAACCG	357		
OY	466	GGCGTGGAGAGCTGCTGGTGAAGTACAGTCCGACGGCATCCGGGGCGCTTGACAG	525		
Db	358	GGCGTGGAGAGCTGCTGGTGAAGTACAGTCCGACGGCATCCGGGGCGCTTGACAG	417		
OY	526	GGCTTCAGTGTCTCCGTGAGGGCATCATCTACCCGGGGCGCTTACTTGGCGGTAC	585		
Db	418	GGCTTCAGTGTCTCCGTGAGGGCATCATCTACCCGGGGCGCTTACTTGGCGGTAC	477		
OY	586	GATACGGCAGAGGGCATGTCTCCCGACCCCAAGAACAGCAGCATGCTGGTAGCTGGATG	645		
Db	478	GATACGGCAGAGGGCATGTCTCCCGACCCCAAGAACAGCAGCATGCTGGTAGCTGGATG	537		
OY	646	ATTCGGCAGACCGTGAAGCGCGCTGGCGCGCGGTGTCTTACCCCTTGCAGACGGTCCG	705		
Db	538	ATTCGGCAGACCGTGAAGCGCGCTGGCGCGCGGTGTCTTACCCCTTGCAGACGGTCCG	597		
OY	706	CGGCGCATGATGATGACGTCGCGGGGCGCAAGAGAGCTGATCATGTACAGGGCAGCGTC	765		
Db	598	CGGCGCATGATGATGACGTCGCGGGGCGCAAGAGAGCTGATCATGTACAGGGCAGCGTC	657		
OY	766	GACTTTGGAGAGAAATCTTTCAGAGATGAGGGGGCAAGGCTTTCCTCAAGGGGTGGTG	825		
Db	658	GACTTTGGAGAGAAATCTTTCAGAGATGAGGGGGCAAGGCTTTCCTCAAGGGGTGGTG	717		
OY	826	TCCAAAGCTTCGGGGGGGAGATGGGGGGCGCGCTGTGCTGCTGTGAGAGAGCTCAAG	885		
Db	718	TCCAAAGCTTCGGGGGGGAGATGGGGGGCGCGCTGTGCTGCTGTGAGAGAGCTCAAG	777		
OY	886	AAGGTGATCTTA 897			
Db	778	AAGGTGATCTTA 789			
RESULT 12					
AX409449	1116 bp	DNA	linear	PAT 14-JUN-2002Z	
LOCUS	AX409449	Sequence 2096 from Patent W00229103.			
DEFINITION	AX409449				
ACCESSION	AX409449.1	GI:21442154			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				

ORGANISM	Homio sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1
TITLE	Alvarez, C., Horne, D., Peraes-da-Silva, S. and Vockley, J.G.
JOURNAL	Gene expression profiles in liver cancer
GENE LOGIC	Patent: WO 0229103-A 2096 11-APR-2002;
FEATURES	GENE LOGIC INC (US)
SOURCE	Location/Qualifiers
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Query Match	86.0%; Score 771.2; DB 6; Length 1116;
Best Local Similarity	99.2%; Pred. No. 4.3e-112;
Matches	786; Conservative 0; Mismatches 3; Indels 3; Gaps 1
QY	106 CTGCAGGTCCAGCAGCCAGCAGCAGATCGCCGCGCAACAGCAGTACAGGGCATCGTG
DB	1 CTGAGGCTCCAGCAGCCAGCAGAGAGATCCCGCCGCAAGCAGTACAGGGCATCGTG
OY	166 GACTGCATATGCCGATATCCCAAGGAGAGGGCGTGCCTTGTGAGGGGCAACCTT
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OY	226 GCCAAGCTCATTTGCTTACTTCCCACTAAGCCCTCAATTCGCTTGAAGATTAAGTAC
DB	121 GCCAAGCTCATTTGCTTACTTCCCACTAAGCCCTCAATTCGCTTGAAGATTAAGTAC
OY	286 AAGCAGATCTTCTGAGGGGGGGGTGGACAGCAGCAGCTTGTGAGGTACTTTCGGGCG
DB	181 AAGCAGATCTTCTGAGGGGGGGGTGGACAGCAGCAGCTTGTGAGGTACTTTCGGGCG
OY	346 AACCTGAGCTCCGGGGGTGGAGCCGGCCGAGCCTCCTCTGCTGTGATCCGCTGGAT
DB	238 AACCTGAGCTCCGGGGGTGGAGCCGGCCGAGCCTCCTCTGCTGTGATCCGCTGGAT
OY	406 TTTCGCCAGACCCGCTGGCAGCGGAGCGTGGGAAAGTACAGGCAGACGCGAGTTCCGA
DB	298 TTTCGCCAGACCCGCTGGCAGCGGAGCGTGGGAAAGTACAGGCAGACGCGAGTTCCGA
OY	466 GGCGTGGAGAGCTGCTGCTGTAAGATACAAATCCAGACGATCCGGGGGCTGTACAG
DB	358 GGCGTGGAGAGCTGCTGCTGTAAGATACAAATCCAGACGATCCGGGGGCTGTACAG
OY	526 GGCTTCAATGCTCTCGTGCAGGGGCTATCATCTACCGGGGGGCTACTTCCGCTGTAC
DB	418 GGCTTCAATGCTCTCGTGCAGGGGCTATCATCTACCGGGGGGCTACTTCCGCTGTAC
OY	586 GATACGGGCAAGGGCATGCTCTCCGACCCCAAGAACAGCAGCATGTGGTGAAGTGATG
DB	478 GATACGGGCAAGGGCATGCTCTCCGACCCCAAGAACAGCAGCATGTGGTGAAGTGATG
OY	646 ATTCGGCAGACGATGACGAGCGGTGGCGGGCGGTGCTTACCCCTTGACACGGGTGGCG
DB	538 ATTCGGCAGACGATGACGAGCGGTGGCGGGCGGTGCTTACCCCTTGACACGGGTGGCG
OY	706 CGGGCGCATGATGATGCTCCGGGGGCAAGAGAGCTGACATCATGTACACGGGACCGTC
DB	598 CGGGCGCATGATGATGCTCCGGGGGCAAGAGAGCTGACATCATGTACACGGGACCGTC
OY	766 GACTGTGTGAGAGAGATCTTCAAGATGAGGGGGCAAGGCTTCTTCAAGGCTGGCTGG
DB	658 GACTGTGTGAGAGAGATCTTCAAGATGAGGGGGCAAGGCTTCTTCAAGGCTGGCTGG
OY	826 TCACAAGCTCTCGGGGAGATGGAGGGGCGCTTCGATGAGGTCTGTGACAGCAGAGCTCAAG
DB	718 TCACAAGCTCTCGGGGAGATGGAGGGGCGCTTCGATGAGGTCTGTGACAGCAGAGCTCAAG

QY	886	AAAGTGATCTAA	897	
Db	778	AAAGTGATCTAA	789	
RESULT 13				
LOCUS	HMMTLCA	1116 bp	mrna	linear
DEFINITION	Human ADP/ATP translocase mRNA, 3' end, clone PHAT8.			PRI 03-AUG-1993
ACCESSION	J03592			
VERSION	J03592.1	GI:339722		
KEYWORDS	ADP/ATP translocase.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 1116)			
TITLE	Houldsworth, J. and Attardi, G.			
	Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 85 (2), 377-381 (1988)			
MEDLINE	88124845			
PUBMED	2829183			
COMMENT	Original source text: Human (adult) liver, cDNA to mRNA, clone PHAT8.			
FEATURES	Draft entry and printed copy of sequence for [1] kindly provided by J.Houldsworth, 04-JAN-1988.			
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BASE COUNT	231 a 330 c 346 g 209 t			
ORIGIN	5 bp upstream of PstI site.			
Query Match	86.0%; Score 771.2; DB 9; Length 1116;			
Best Local Similarity	99.2%; Pred. No. 4.3e-112;			
Matches 786; Conservative	0; Mismatches 3; Indels 3; Gaps 1;			
QY	106	CTGCAGGTCGACAGCGACGACAGACAGATGCGCGCCGACGACGATCAAGGCGATG	165	
Db	1	CTGCAGGTCGACAGCGACGACAGATGCGCGCGCCGACGACGATCAAGGCGATG	60	
QY	166	GACTGCATGTGCGCATCCCAAGAGGAGGCGTGTCTTCCTTGAGGGGCAACTT	225	
Db	61	GACTGCATGTGCGCATCCCAAGAGGAGGCGTGTCTTCCTTGAGGGGCAACTT	120	
QY	226	GCCACAGTCATTCGCTACTTCCCACTCAACCCCTCAACTTCGCGCTTCAAGATAAGTAC	285	
Db	121	GCCACAGTCATTCGCTACTTCCCACTCAACCCCTCAACTTCGCGCTTCAAGATAAGTAC	180	
QY	286	AAGCAGATCTTCTGAGGGGCGTGGAGACAAAGCAGCAGTTCGTGAGGATCTTGGCGGC	345	
Db	181	AAGCAGATCTTCTGAGGGGCGTGGAGACAAAGCAGCAGTTCGTGAGGATCTTGGCGGC	237	
QY	346	AACCTGCGCTCGGGGCGTGGAGCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGAT	405	
Db	238	AACCTGCGCTCGGGGCGTGGAGCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGAT	297	
QY	406	TTTGGCAGAACCCCGCTGGCAGCGCAGCTGGGAAAGTCAGGCACAGACCGGAGTTCCGA	465	
Db	298	TTTGGCAGAACCCCGCTGGCAGCGCAGCTGGGAAAGTCAGGCACAGACCGGAGTTCCGA	357	

OY		466	GCCCTGGGGAACAGCCTCGTGTAAATCAACAAGTCGCAGCGCATCCGGGGCGCTGTACAG	525
Db		358	GGCCCTGGGAACACTCGTGTTGAATCACCAAGTCGACGCCATCCGGGGCGCTGTACAG	417
OY		526	GGCTTCAGTGTCTCCGTGACAGCCATCATCTACCGGGGGCGCTACTTGGCGGTTC	585
Db		418	GGCTTCAGTGTCTCGTGTACAGGCATCATCTACCGGGGGCGCTACTTGGCGGTTC	477
OY		586	GATTACGGGCGAAGGGCATGTCCTCCCCAACCCCAAAGAACCACATCTGTGACCTTAGG	645
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OY		646	ATCCGCGACACCGTCAGCGCCCGTGGCCGGCTGTCTCTACCCCTTTCAGACGGTGGC	705
Db		538	ATCCGCGACACCGTCAGCGCCCGTGGCCGGCTGTCTCTACCCCTTTCAGACGGTGGC	597
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Db		598	CGGGCGATGATGTGTCAGTCCGGGGCGCAAAAGACGTACATCATGTACACGGGACCGTC	657
OY		766	GACTGTGTGGAGAGATCTTCAGACATGAGGGGGCGCAAGCCCTTCTTCAGAGGTGGTGG	825
Db		658	GACTGTGTGGAGAGATCTTCAGACATGAGGGGGCGCAAGCCCTTCTTCAGAGGTGGTGG	717
OY		826	TCCAACTCTCTCGGGGGGATGAGGGGGCGCCCTTGCTGCTGCTGTACGACGAGCTCAAG	885
Db		718	TCCAACTCTCTCGGGGGGATGAGGGGGCGCCCTTGCTGCTGCTGTACGACGAGCTCAAG	777
OY		886	AAGGTGATCTTA 897	
Db		778	AAGGTGATCTTA 789	
RESULT 14				
AC125887/c				
LOCUS				
DEFINITION				
AC125887			291762 bp DNA linear HTG 15-NOV-2002	
AC125887			Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS	
AC125887_3			GI:25008671	
HTG:			HTGS_PHASE1: HTGS_DRAFT; HTGS_ENRICHED.	
KEYWORDS			Rattus norvegicus (Norway rat)	
SOURCE			Rattus norvegicus	
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
			Rattus;	
REFERENCE			1 (bases 1 to 291762)	
AUTHORS			Muzny,D.,Marrie,L.,Metzger,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,	
			Allan,C.,Allen,H.,Alsbrooks,S.,Amis,A.,Angiano,D.,	
			Anylebech,I.,Ayodeji,A.,Ayodeji,M.,Baca,E.,Baden,H.,	
			Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benmehd,F.,	
			Biswalto,K.,Blair,J.,Blankenburg,K.,Blythe,P.,Brown,M.,	
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			Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,	
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			Devalla,M.L.,Davis,S.,Davy-Carroll,L.,De Andra,C.,Deedrich,D.,	
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			Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,T.,Garza,M.,	
			Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Gerret,T.,Garza,M.,	
			Gebregorgis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,M.,Guerra,W.,	
			Gunaratne,P.,Haaland,W.,Hamli,C.,Hamilton,C.,Hamilton,K.,	
			Harvey,Y.,Havlik,P.,Hawes,A.,Henderson,N.,Hernandez,J.,	
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			Kowalski,C.,Kraft,C.L.,Ledow,H.,Levan,J.J.,Lewis,L.,Li,Z.,Liu,J.,	
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			Lorenswahl,M.,Louisaged,H.,Lozano,R.J.,Lu,X.,Ma,J.,	
			Maheshwari,M.,Mainimadine,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,	

Maqum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhinney,S., McLeod,M.P., McNally,T.Z., Meenen,E.,
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Narkewicz,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwokilemech,O., Okunolu,G., Olamugboye,A., Pal,S.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfankuch,C.,
Plopper,F., Polidexter,A., Popovtch,D., Plums,E., Pu,L.,
Puzio,M., Quirroz,C., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,T., Reuter,M., Richards,S., Riggs,F.,
Sanders,W., Savary,D., Scherer,S., Scott,G., Shatman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C., Smaljs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sotelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Swatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tringola,A., Trogos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleciwyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,Y.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., Von
Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 291762)

Worley,K.C.

Direct Submission
Submitted (02-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 291762)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23269681.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rac/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
collisions within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center -----
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: GMD
Center Clone name: CH230-77403
----- Summary Statistics -----
Assembly program: Phrap: version 0.990329
Consensus quality: 220653 bases at least Q40
Consensus quality: 230853 bases at least Q30
Consensus quality: 233437 bases at least Q20
Estimated insert size: 233445, sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

Mon Aug 25 09:31:42 2003

us-09-811-094-3.rge

Page 14

FEATURES	Location/Qualifiers
left end of clone RP11-27103	is at 128593 in this sequence. The
true right end of clone RP11-69715	is at 36723 in this sequence

FEATURES	Location/Qualifiers
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ORIGIN								

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Matches 793; Conservative 0; Mismatches 74; Indels 24; Gaps 2;

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Db 103170 ATGACGACAAGCCATCTCCTTCGCCAAGGACTTCCCTAGCTGGAGGCATCACC GCCCT 103229

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Db 103230 ATCTCAAGACAGCCGTCGATCGATCAAGCGGTCACGCTGCTGCTGCAGATGCAGCAC 103289

121 GCCAGCAAGCAGATCGCCCGACACAGCAGTACAAAGGCATCGTGGACTGCATTGTCCGC 180

Db 103290 GCCAGCATGCCGATGGCCCGCCAGCAGTGC AAGGCATCGTGACTGCATCGTCCGC 103349

181 ATCCCAAGGAGGCGTGTCTTCTGGAGGGCAACCTTGCCAACGTCATTCCG 240

Db 103350 ATCCCAAGATCAGGGCGTGTCTTCTCTGAGGGGCAACCTGGCCAATGTCATCCGC 103409

241 TACTTCCCACTCAAGCCCTCAACTTCGCCTCAAGGATAAGTACAAGCAGATCTTCCTG 300

Db 103410 TACTCCCCCAGCAGCCCTCATTTGCGCTTCAAGGATAAGTACAGCAGATCTTCCTG 103469

301 GGGGCGTGACACGACACGAGTCTGGAGTACTTTGGGGCAACCTGGCCTCCGGC 360

Db 103470 GCGGCGTGACACACGAGTCTGCGAGTACTTTGGGGCAACCTGGCTTGGC 103529

361 GGTGCGCGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTCGCCAGAACCCGC 420

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 00:45:07 ; Search time 314 Seconds

(without alignments)
7711.452 Million cell updates/sec

Title: US-09-811-094-3

Perfect score: 897
Sequence: 1 atgacgcgaacagccatctc.....agctcaagaagtgatctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
- 5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
- 6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
- 9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
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- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	897	100.0	897	21	AAD00521	Human adenine nucl
2	897	100.0	897	22	AAS05903	Human adenine nucl
3	897	100.0	897	22	AAI16690	DNA encoding human
4	895.4	99.8	1212	22	AAI58797	Human polynucleoti
5	895.4	99.8	2035	22	AAI60583	Human polynucleoti
6	873.4	97.4	2592	22	ABX63152	Human cDNA #152 di
7	816.4	91.0	2213	25	ACC46652	Human dittp organe
8	771.2	86.0	1116	24	ABK83761	Human cDNA differe

9	771.2	86.0	1116	24	ABN95598	Gene #2096 used to
10	771.2	86.0	1116	24	ABL69347	Prostate cancer re
11	647.4	72.2	687	24	ABO56282	Human ovarian anti
12	596.2	66.5	1196	24	ABK63420	Rat sequence diffe
13	596.2	66.5	1225	24	AAI48635	Human insulin rece
14	594.6	66.3	897	21	AAD00520	Human adenine nucl
15	594.6	66.3	897	22	AAS05902	Human adenine nucl
16	594.6	66.3	897	24	AAI16689	DNA encoding human
17	591.4	65.9	1259	19	AAV36480	Ant1 cDNA. Mus sp
18	588.2	65.6	1177	19	AAV36479	Ant1 cDNA. Mus sp
19	568.4	63.4	1156	23	AAI91243	DNA encoding novel
20	564.2	62.9	894	21	AAD00519	Human adenine nucl
21	564.2	62.9	894	22	AAS05901	Human adenine nucl
22	564.2	62.9	894	22	AAI16688	DNA encoding human
23	564.2	62.9	1024	25	ABZ83302	Toxicologically re
24	564.2	62.9	1320	24	ABZ56029	Invertebrate forag
25	550.4	61.4	669	24	ABZ33737	Human TRICH encodi
26	519.2	57.9	1581	23	ABL18531	Drosophila melanog
27	519.2	57.9	1750	23	ABL20867	Drosophila melanog
28	482.4	53.8	2706	22	AAS29836	Human cytoskeletal
29	482.4	53.8	2706	22	AAS35083	Human cDNA differe
30	482.4	53.8	220895	24	ABK84798	Drosophila melanog
31	462.6	51.6	1033	23	ABL03127	DNA encoding novel
32	406.6	45.3	943	24	ABN74319	Human TRICH-19 CDN
33	400.8	44.7	1251	23	AAI79610	DNA encoding novel
34	394	43.9	720	24	ABZ76857	Frog embryonic gen
35	394	43.9	720	24	ABZ76857	Frog embryonic gen
36	363	40.5	1455	23	AAS68190	DNA encoding novel
37	354.4	39.5	1781	24	AAD33664	Human TRICH-19 CDN
38	354.4	39.5	1803	23	ABX71399	Human metabolizm-a
39	344.6	38.4	5407	23	ABL18530	Drosophila melanog
40	344.6	38.4	8031	23	ABL20966	Drosophila melanog
41	338.8	37.8	698	24	ABT09322	Phase-1 Rat CT gen
42	332.2	37.0	989	24	ABN74435	Bovine embryonic g
43	325.6	36.3	5768	24	ABL61797	Colton adenocarcino
44	322.6	36.0	731	20	AAK39617	Breast cancer asso
45	318.6	35.5	434	25	ABX47259	Bovine EST associa

ALIGNMENTS

RESULT 1	
AAD00521	
ID	AAD00521 standard; cDNA: 897 BP.
XX	
AC	AAD00521;
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human adenine nucleotide translocator ANT3 cDNA.
XX	
KW	Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotoxic;
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiposrotatic; cerebroprotective; therapeutic; screening; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIRD;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
XX	1..897
XX	/*tag- a
XX	/product- "ANT3"
XX	MO200026370-A2.
PD	11-MAY-2000.

XX 03-NOV-1999; 99MO-US25883.
XX 03-NOV-1998; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX (MITO-) MITOKOR.
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh S;
XX MPI: 2000-365619/31.
XX F-PSDB; AAT171033.
XX Recombinant construct encoding adenine nucleotide translocator
XX against mitochondrial disease -
XX
XX Example 1: Page 166; 175pp; English.
XX The patent discloses a method to produce adenine nucleotide translocator
XX (ANT) proteins or ANT fusion proteins using recombinant expression of
XX constructs. ANT is a nuclear encoded protein and a major component of
XX inner mitochondrial membrane. It mediates transport of adenosine
XX di/tri-phosphates across the mitochondrial inner membrane and also serves
XX as an important molecular component of the mitochondrial permeability
XX transition pore, a modulator of apoptosis. ANT is used to identify agents
XX or ligands that bind to, or interact with it. The ANT ligands are used to
XX detect or isolate ANT in a biological sample, and therapeutically for
XX regulating mitochondrial pore activity, for treating diseases associated
XX with altered mitochondrial function, including Alzheimer's, Parkinson's
XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
XX disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
XX epilepsy red ragged fibre syndrome. The present sequence is a cDNA
XX encoding adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other:
SQ
Query Match 100.0%; Score 897; DB 21; Length 897;
Best local similarity 100.0%; Pred. No. 1.3e-175;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGGAACAGGCGCATCTCTCGCAAGACTTCTTGCGCGAGGACATCCGCGCGC 60
DB 1 ATGAGGGAACAGGCGCATCTCTCGCAAGACTTCTTGCGCGAGGACATCCGCGCGC 60
QY 61 ATCTCCAGAGCGCGCGTGGCTCGATCGAGCGGGTCAAGCTGCTGCAGGTCCAGCAC 120
DB 61 ATCTCCAGAGCGCGCGTGGCTCGATCGAGCGGGTCAAGCTGCTGCAGGTCCAGCAC 120
QY 121 GCCACAGAGAGATCGCGCGCGACAAAGAGTCAAGGGCATCTGAGTGTCTCCGC 180
DB 121 GCCACAGAGAGATCGCGCGCGACAAAGAGTCAAGGGCATCTGAGTGTCTCCGC 180
QY 181 ATCCCAAGAGAGAGCGCGCGTGTCTCTTGAGAGGGCAACCTTGGCAAGGTATTCGC 240
DB 181 ATCCCAAGAGAGAGCGCGCGTGTCTCTTGAGAGGGCAACCTTGGCAAGGTATTCGC 240
QY 241 TACTTCCCACTCAAGCCCTCACTTGGCTTCAAGATTAAGTACAAGAGATCTTCTCG 300
DB 241 TACTTCCCACTCAAGCCCTCACTTGGCTTCAAGATTAAGTACAAGAGATCTTCTCG 300
QY 301 GGGGGCGTGGAGCAAGCAAGCAAGTCTGAGAGTACTTGGGGCAACCTGGCTCCGCG 360
DB 301 GGGGGCGTGGAGCAAGCAAGCAAGTCTGAGAGTACTTGGGGCAACCTGGCTCCGCG 360
QY 361 GGTGGCGCGCGCGAGCTCTCTGCTGTGATCCCGCTGATTTTGGCAGAACCCGCG 420
DB 361 GGTGGCGCGCGCGAGCTCTCTGCTGTGATCCCGCTGATTTTGGCAGAACCCGCG 420
QY 421 CTGGCAGCGAGCTGTGGAAAGTCAAGCAGAGCGCGAGTTCGAGGCGTGGAGACTGC 480

DB 421 CTGGCAGCGAGCTGTGGAAAGTCAAGCAGAGCGCGAGTTCGAGGCGTGGAGACTGC 480
QY 481 CTGGTGAAGATCACCAAGTCCGAGCGCATCCGGGGCTGTACAGAGGCTTCATGTCTCC 540
DB 481 CTGGTGAAGATCACCAAGTCCGAGCGCATCCGGGGCTGTACAGAGGCTTCATGTCTCC 540
QY 541 GTGCAAGGATCATCATCTACCGGGGGCTACTTGGCGGTACGATAGGCGCAAGGCG 600
DB 541 GTGCAAGGATCATCATCTACCGGGGGCTACTTGGCGGTACGATAGGCGCAAGGCG 600
QY 601 ATGCTCCCGAGCCCAAGAACAGCGACATCGTGTGACGTGATCGGCGAGACCGTG 660
DB 601 ATGCTCCCGAGCCCAAGAACAGCGACATCGTGTGACGTGATCGGCGAGACCGTG 660
QY 661 ACGGCGGTGGCGCGCGTGTCTGCTACCGCTTCGACACGGTGGCGCGCATGATGATG 720
DB 661 ACGGCGGTGGCGCGCGTGTCTGCTACCGCTTCGACACGGTGGCGCGCATGATGATG 720
QY 721 CAGTCCGGCGCAAGAGAGCTGACATCATGATACAGCGGACCGTGCATGTGGAGGAAG 780
DB 721 CAGTCCGGCGCAAGAGAGCTGACATCATGATACAGCGGACCGTGCATGTGGAGGAAG 780
QY 781 ATCTTCAGAGATGAGGGGGCAAGGCGCTTCTTCAAGGGGTGCGTCAACGTCGCGG 840
DB 781 ATCTTCAGAGATGAGGGGGCAAGGCGCTTCTTCAAGGGGTGCGTCAACGTCGCGG 840
QY 841 GGCATGGGGGGCGCTTCTGCTGTCTGTACGAGAGCTCAAGAGTGAATCTTA 897
DB 841 GGCATGGGGGGCGCTTCTGCTGTCTGTACGAGAGCTCAAGAGTGAATCTTA 897
RESULT 2
AAS05903 standard; cDNA; 897 BP.
ID AAS05903
XX AAS05903;
XX
XX 07-SEP-2001 (first entry)
XX
XX Human adenine nucleotide translocator-3 (ANT-3) cDNA sequence.
DE
XX
XX Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 1..897
FT CDS /tag= a
FT /product= "ANT-3"
XX
XX WO200132876-A2.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000MO-US30535.
XX
XX 03-NOV-1999; 99US-0434354.
XX
XX (MITO-) MITOKOR.
XX
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Erliger LG;
PI Veliczelebi G, Davis RE;
XX
XX MPI: 2001-291054/30.
XX F-PSDB; AAD01200.
XX
XX New nucleic acid expression constructs, useful for screening for agents
XX that alter mitochondrial permeability transition (MPT), comprises
XX polynucleotide encoding MPT polypeptide or cyclophilin polypeptide

PT fused to energy transfer molecule -
 PS Disclosure; Fig 1; 186pp; English.
 XX
 CC The present sequence encodes for human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX

SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other;

Query Match 100.0%; Score 897; DB 22; Length 897;
 Best Local Similarity 100.0%; Pred. No. 1.3e-175;

Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGAACAGAGCCATCTCTTCCTTCCGCAAGACATTCTTGGCGGAGCATCCGCCGCC 60
 DB 1 ATGAGGGAACAGAGCCATCTCTTCCTTCCGCAAGACATTCTTGGCGGAGCATCCGCCGCC 60
 QY 61 ATCTCCAAAGACGGCGCTGCTCCGATCGAGCGGGGTCAAGCTGCTGCGAGGTCAGCAG 120
 DB 61 ATCTCCAAAGACGGCGCTGCTCCGATCGAGCGGGGTCAAGCTGCTGCGAGGTCAGCAG 120
 QY 62 ATCTCCAAAGACGGCGCTGCTCCGATCGAGCGGGGTCAAGCTGCTGCGAGGTCAGCAG 120
 DB 62 ATCTCCAAAGACGGCGCTGCTCCGATCGAGCGGGGTCAAGCTGCTGCGAGGTCAGCAG 120
 QY 121 GCCAGCAAGCAGATGCGCGCCGACAAAGAGTACAAAGGCGATGCTGAGTCAATTTGCCG 180
 DB 121 GCCAGCAAGCAGATGCGCGCCGACAAAGAGTACAAAGGCGATGCTGAGTCAATTTGCCG 180
 QY 122 GCCAGCAAGCAGATGCGCGCCGACAAAGAGTACAAAGGCGATGCTGAGTCAATTTGCCG 180
 DB 122 GCCAGCAAGCAGATGCGCGCCGACAAAGAGTACAAAGGCGATGCTGAGTCAATTTGCCG 180
 QY 181 ATCCCAAGAGGAGCGGGCTGCTCTTCTGAGGGGCAACCTTCCAAAGTCATTCGCG 240
 DB 181 ATCCCAAGAGGAGCGGGCTGCTCTTCTGAGGGGCAACCTTCCAAAGTCATTCGCG 240
 QY 182 ATCCCAAGAGGAGCGGGCTGCTCTTCTGAGGGGCAACCTTCCAAAGTCATTCGCG 240
 DB 182 ATCCCAAGAGGAGCGGGCTGCTCTTCTGAGGGGCAACCTTCCAAAGTCATTCGCG 240
 QY 241 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGATTAAGTACAGAGATCTTCGCG 300
 DB 241 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGATTAAGTACAGAGATCTTCGCG 300
 QY 301 GGGGGCGTGGACAGACAGCAGTTCGAGGTACTTTCGCGGCAACCTTGGCCTCCGCG 360
 DB 301 GGGGGCGTGGACAGACAGCAGTTCGAGGTACTTTCGCGGCAACCTTGGCCTCCGCG 360
 QY 361 GGTGGCGGGCGGCGCACTCCCTCTGCTTCTGATCCGCTGGATTTCCAGAAACCCGC 420
 DB 361 GGTGGCGGGCGGCGCACTCCCTCTGCTTCTGATCCGCTGGATTTCCAGAAACCCGC 420
 QY 421 CTGGCAGCGGAGCTGGGAAAGTCAGGACAGACGCGGAGTTCGAGGCGCTGGAGACTGC 480
 DB 421 CTGGCAGCGGAGCTGGGAAAGTCAGGACAGACGCGGAGTTCGAGGCGCTGGAGACTGC 480
 QY 481 CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 DB 481 CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 QY 541 GTGCGAGGATATATATCTAACGGGGGCTTACTTGGCGGTGATACATTCGCGCAAGGCG 600
 DB 541 GTGCGAGGATATATATCTAACGGGGGCTTACTTGGCGGTGATACATTCGCGCAAGGCG 600
 QY 601 ATGCTCCCGGACCCCAAGAACAGCAGCATGCTGAGTGAAGTGAATTCGCGCAGACGCTG 660
 DB 601 ATGCTCCCGGACCCCAAGAACAGCAGCATGCTGAGTGAAGTGAATTCGCGCAGACGCTG 660

QY 661 ACGGCGGTGGCGGCGCTGTCTTCTACCCCTTGCACACGTGGCGGCGCATGATGATG 720
 DB 661 ACGGCGGTGGCGGCGCTGTCTTCTACCCCTTGCACACGTGGCGGCGCATGATGATG 720
 QY 721 CAGTCCGGGCGCAAGAGACTGATCATCATGATACACGGGACCGTGCATCTTTGGAGGA 780
 DB 721 CAGTCCGGGCGCAAGAGACTGATCATCATGATACACGGGACCGTGCATCTTTGGAGGA 780
 QY 781 ATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGCGTCAACGTCCTGCGG 840
 DB 781 ATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGCGTCAACGTCCTGCGG 840
 QY 841 GGCATGAGATGAGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 DB 841 GGCATGAGATGAGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

RESULT 3

AA16690 standard; cDNA; 897 BP.
 ID AA16690 standard; cDNA; 897 BP.
 AC AA16690;

DT 14-FEB-2002 (first entry)

DE DNA encoding human adenine nucleotide translocator 3 (ANT3).

XX Human: adenine nucleotide translocator; ANT; ss;

KW mitochondrial matrix protein.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..897

FT /tag a /product="adenine nucleotide translocator 3 (ANT3)"

PN MO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001MO-US15416.

XX 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Cleveanger W, Wiley SE, Miller SM, Szabo TR;

XX Ghosh SS, Moos WH, Pel Y, Carroll AK;

XX WPI: 2002-055598/07.

XX P-P-SDB; AAU10380.

XX Novel recombinant expression construct for producing adenine nucleotide

XX translocator polypeptides, comprises a regulated promoter linked to

XX nucleic acid encoding the polypeptide

XX Example 3; Fig 1; 147pp; English.

XX The invention relates to a recombinant expression construct (I)

XX comprising a regulated promoter operably linked to a nucleic acid

XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT

XX proteins mediate the exchange of ATP synthesized in the mitochondrial

XX matrix for ADP in the cytosol. (I) is useful for producing recombinant

XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and

XX culturing the host cell. (I) is also useful for targeting a polypeptide

XX of interest to a mitochondrial membrane, where ANT polypeptide is

XX expressed as a fusion protein with the polypeptide of interest.

XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is

XX useful for identifying an agent that binds to an ANT polypeptide. ANT

XX ligand is useful for determining the presence of an ANT polypeptide,

XX preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-
covalently bound to a solid phase. Detectably labeled ANT ligand is also
useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the coding sequence of human ANT3.
XX
XX Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other:

Query Match 100.0%; Score 897; DB 24; Length 897;
Best Local Similarity 100.0%; Pred. No. 1.3e-175;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTTGGCCGAGAGCATCCGCCGCC 60
1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTTGGCCGAGAGCATCCGCCGCC 60
61 ATCTCCAAAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
61 ATCTCCAAAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
121 GCCAGCAGCAGATCGCCGCCGACAGCAGTACAGGAGCATCTGAGCTGATCTGCCG 180
121 GCCAGCAGCAGATCGCCGCCGACAGCAGTACAGGAGCATCTGAGCTGATCTGCCG 180
181 ATCCCAAGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
181 ATCCCAAGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGAGTAAAGTACAAAGAGATCTTCTG 300
241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGAGTAAAGTACAAAGAGATCTTCTG 300
301 GGGGGCGTGGACAGCAGCAGTCTGAGAGTACTTGGCGGCAACCTGACCTCCGCGC 360
301 GGGGGCGTGGACAGCAGCAGTCTGAGAGTACTTGGCGGCAACCTGACCTCCGCGC 360
361 GGTGGCGCGCGGAGCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 GGTGGCGCGCGGAGCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 CTGGAGAGGAGCGTGGGAAAGTCAGGACAGAGCGCGAGTTCGAGAGCCTGGGAGAC 480
421 CTGGAGAGGAGCGTGGGAAAGTCAGGACAGAGCGCGAGTTCGAGAGCCTGGGAGAC 480
481 CTGGGAAAGTACACCAAGTCCGAGCGCATCCGGGCGCTTACAGGCGCTTCAAGTCTCC 540
481 CTGGGAAAGTACACCAAGTCCGAGCGCATCCGGGCGCTTACAGGCGCTTCAAGTCTCC 540
541 GTGAGAGGCGCATCTACCGGGCGCTTACCTTGGCGCTTACAGTACGCGCAAGGCG 600
541 GTGAGAGGCGCATCTACCGGGCGCTTACCTTGGCGCTTACAGTACGCGCAAGGCG 600
601 ATGTCCCGCCAGCCCAAGAACAGCAGCATCTGCTGAGCTGAGTATCCGAGACCTGG 660
601 ATGTCCCGCCAGCCCAAGAACAGCAGCATCTGCTGAGCTGAGTATCCGAGACCTGG 660
661 ACGGCGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
661 ACGGCGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
721 CAGTCCGCGGCAAAAGAGCTGACATCATGTATACAGGCGCCTGACGTGTGGAGAG 780
721 CAGTCCGCGGCAAAAGAGCTGACATCATGTATACAGGCGCCTGACGTGTGGAGAG 780
781 ATCTTCAGAGTATGAGGGGGCAAGGCTTCTTCAAGGGTGCAGGCTCCTGCGG 840
781 ATCTTCAGAGTATGAGGGGGCAAGGCTTCTTCAAGGGTGCAGGCTCCTGCGG 840
841 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
841 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897

RESULT 4

AA158797
ID AA158797 standard; cDNA; 1212 BP.
AC AA158797;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 1000.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukemia; ss.
XX Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000MO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI: 2001-442253/47.
XX P-PSDB: AAM39641.

XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 1000; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cyostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukemia and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.

XX Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 other:

Query Match 99.8%; Score 895.4; DB 22; Length 1212;
Best Local Similarity 99.9%; Pred. No. 2.8e-175;
Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTTGGCCGAGAGCATCCGCCGCC 60
131 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTTGGCCGAGAGCATCCGCCGCC 190

QY 61 ATCTCAAGAGCGCGGTGGCTCCATCGAGCGGGTCAAGCTGTCTGTGAGGTCCAGCAC 120
 XX |||||
 OS 191 ATCTCAAGAGCGCGGTGGCTCCATCGAGCGGGTCAAGCTGTCTGTGAGGTCCAGCAC 250
 XX |||||
 PN 121 GCCAGCAGAGATGCGCGCGGACAGAGATCAAGGGCATGCTGAGTGTCTCCGC 180
 XX |||||
 PD 251 GCCAGCAGAGATGCGCGCGGACAGAGATCAAGGGCATGCTGAGTGTCTCCGC 310
 XX |||||
 PF 181 ATCCCAAGAGAGAGCGGTGCTGTCTGTGAGGGGCAACCTTGCCAACTCATTTCCG 240
 XX |||||
 PR 311 ATCCCAAGAGAGAGCGGTGCTGTCTGTGAGGGGCAACCTTGCCAACTCATTTCCG 370
 XX |||||
 QY 241 TACTTCCCACTCAAGCCCTCACTTGTGCTTCAAGATTAAGTACAGAGATCTTCTG 300
 XX |||||
 DB 371 TACTTCCCACTCAAGCCCTCACTTGTGCTTCAAGATTAAGTACAGAGATCTTCTG 430
 XX |||||
 QY 301 GGGGGCGTGGACACAGCAGATGTTGAGAGTCTTTGGCGGCACCTGGCTCCGGC 360
 XX |||||
 DB 431 GGGGGCGTGGACACAGCAGATGTTGAGAGTCTTTGGCGGCACCTGGCTCCGGC 490
 XX |||||
 QY 361 GGTGGCGCGGCGGACCTCCCTGTCTGTGCTGTACCCGCTGATTTTGGCCAGAACCCGC 420
 XX |||||
 DB 491 GGTGGCGCGGCGGACCTCCCTGTCTGTGCTGTACCCGCTGATTTTGGCCAGAACCCGC 550
 XX |||||
 QY 421 CTGGCAGCGGAGCTGGGAAAAGTCAAGCAGACAGCCGAGATTCCGAGGCTGGAGACTGC 480
 XX |||||
 DB 551 CTGGCAGCGGAGCTGGGAAAAGTCAAGCAGACAGCCGAGATTCCGAGGCTGGAGACTGC 610
 XX |||||
 QY 481 CTGGTGAAGATACCAAGTCCGAGCGGACATCCGGGGCTGTACACAGGGCTTCAAGTCTTC 540
 XX |||||
 DB 611 CTGGTGAAGATACCAAGTCCGAGCGGACATCCGGGGCTGTACACAGGGCTTCAAGTCTTC 670
 XX |||||
 QY 541 GTGACGGGCATCATCATCTACCGGGCGCTTCTTCTGCGGTGTACGATACGCCCAAGGGC 600
 XX |||||
 DB 671 GTGACGGGCATCATCATCTACCGGGCGCTTCTTCTGCGGTGTACGATACGCCCAAGGGC 730
 XX |||||
 QY 601 ATGCTCCCGGACCCCAAGAACAGCAGATCTGTGTGAGCTGATGTGCGCAGACCGTG 660
 XX |||||
 DB 731 ATGCTCCCGGACCCCAAGAACAGCAGATCTGTGTGAGCTGATGTGCGCAGACCGTG 790
 XX |||||
 QY 661 ACGGCGTGGCGCGGCTGTGCTTACGCCCTTGCAGACGCGTGGCGGCGCATGTGATG 720
 XX |||||
 DB 791 ACGGCGTGGCGCGGCTGTGCTTACGCCCTTGCAGACGCGTGGCGGCGCATGTGATG 850
 XX |||||
 QY 721 CAGTCCGGGCGCAAGAGAGCTGACATCATGTACAGCGGACCGTGCATGTTGAGAGAG 780
 XX |||||
 DB 851 CAGTCCGGGCGCAAGAGAGCTGACATCATGTACAGCGGACCGTGCATGTTGAGAGAG 910
 XX |||||
 QY 781 ATCTTCAAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGTGCTTCAAGCTGTGCGG 840
 XX |||||
 DB 911 ATCTTCAAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGTGCTTCAAGCTGTGCGG 970
 XX |||||
 QY 841 GGCATGGGGGGGCGCTTGTGCTGTGCTGTACGAGCGAGCTCAAGAGGTGATCTTA 897
 XX |||||
 DB 971 GGCATGGGGGGGCGCTTGTGCTGTGCTGTACGAGCGAGCTCAAGAGGTGATCTTA 1027
 XX |||||

RESULT 5
 AA160583/c
 ID AA160583 standard: cDNA: 2035 BP.

AA160583;
 22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4572.

Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 peripheral nervous system; neuropathy; central nervous system; CNS;
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW 1 leukemia; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0596042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao Q, Zhou P, Goodrich R, Dymnac RT;
 XX
 DR WPI: 2001-442253/47.
 XX
 PS P-PSDB: AAM41427.
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 Claim 1; SEQ ID NO 4572; 10078bp; English.
 XX
 The invention relates to human nucleic acids (AA157798-AA161369) and
 the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 system, such as peripheral nervous injuries, peripheral neuropathy and
 localized neuropathies and central nervous system diseases, such as
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 utilisation of the activities such as: immune system suppression,
 activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 assays for receptor activity, arthritis and inflammation, leukemias and
 C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 SQ Sequence 2035 BP; 398 A; 611 C; 625 G; 401 T; 0 other;
 XX
 Query Match 99.8%; Score 895.4; DB 22; Length 2035;
 Best Local Similarity 99.8%; Pred. No. 3e-175;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGACGGAACAGGCGCATCTCTTCCGCAAGACTTCTTGGCGGAGCATCCCGCGCC 60
 DB 1932 ATGACGGAACAGGCGCATCTCTTCCGCAAGACTTCTTGGCGGAGCATCCCGCGCC 1873
 QY 61 ATCTCCAGAGCGCGGTGCTCGATCGAGCGGGTCAAGCTGCTGTGAGTCCAGCAC 120
 DB 1872 ATCTCCAGAGCGCGGTGCTCGATCGAGCGGGTCAAGCTGCTGTGAGTCCAGCAC 1813
 QY 121 GCGAGCAACAGATGCGCGCGGACAGAGCTCAAGGGGATGTGACATGTCGCGC 180
 DB 1812 GCGAGCAACAGATGCGCGCGGACAGAGCTCAAGGGGATGTGACATGTCGCGC 1753
 QY 181 ATCCCAAGAGAGAGCGGTGCTGTGCTTCTGAGGGGCAACTTGCACATCTTCCG 240
 DB 1752 ATCCCAAGAGAGAGCGGTGCTGTGCTTCTGAGGGGCAACTTGCACATCTTCCG 1693
 QY 241 TACTTCCCACTCAAGCCCTCACTTGTGCTTCAAGATTAAGTACAGAGATCTTCTG 300

DB 1692 TACTTCCCACTGACACCCCTCACTGCGCTCAAGATATGACAGAGATCTCTCCTG 1633
 QY 301 GGGGGGCTGACACACACACAGCTTGTGAGTACTTTGGGGGACCTGGCCCTCCGGC 360
 DB 1632 GGGGGGCTGACACACACACAGCTTGTGAGTACTTTGGGGGACCTGGCCCTCCGGC 1573
 QY 361 GGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 DB 1572 GGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1513
 QY 421 CTGGCAGCGGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCGAGAGCTGGAGACCTG 480
 DB 1512 CTGGCAGCGGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCGAGAGCTGGAGACCTG 1453
 QY 481 CTGGTGAAGATCAACAGTCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 DB 1452 CTGGTGAAGATCAACAGTCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1393
 QY 541 GTGCAAGGATCAACAGTCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 DB 1392 GTGCAAGGATCAACAGTCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1333
 QY 601 ATGCTCCCGACCCCAAGAACACGACATCGTGTGAGTGTGATGATGCGGACACCGCTG 660
 DB 1332 ATGCTCCCGACCCCAAGAACACGACATCGTGTGAGTGTGATGATGCGGACACCGCTG 1273
 QY 661 ACGGCGCTGGCGCGCTGTGTCTTACCCCTTGCACACGAGTGGCGGCGGCGGCGGCGGCGG 720
 DB 1272 ACGGCGCTGGCGCGCTGTGTCTTACCCCTTGCACACGAGTGGCGGCGGCGGCGGCGGCGG 1213
 QY 721 CAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 DB 1212 CAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1153
 QY 781 ATCTTCAGAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 DB 1152 ATCTTCAGAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1093
 QY 841 GGCATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 897
 DB 1092 GGCATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1036

RESULT 6
 ID ABX63152 standard; cDNA; 2592 BP.
 AC ABX63152;
 XX 25-FEB-2003 (first entry)
 DE Human cDNA #152 differentially expressed in activated vascular tissue.
 KW Human; gene; ss; vascular tissue; cytosolic; atherosclerosis;
 KW cardiant; hypotensive; antidiabetic; gynaecological; vasodilator;
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 KW Ischemia-reperfusion injury; stroke;
 XX Homo sapiens.
 OS
 XX US2002137081-A1.
 PN
 XX 26-SEP-2002.
 PD
 XX 08-JAN-2002; 2002US-0044090.
 PE
 XX 28-JUL-2000; 2000US-222469P.
 PR
 XX 08-JAN-2001; 2001US-260483P.
 XX (BAND/) BANDMAN O.
 XX

PI Bandman O;
 XX WPI: 2003-110597/10.
 DR
 XX Combination for diagnosing, staging, treating, or monitoring the
 PR progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several cDNAs that are differentially expressed in activated
 XX vascular tissue -
 XX
 PS Claim 1; Page -; 18pp; English.
 CC This invention relates to a combination comprising several cDNAs that
 CC are differentially expressed in activated vascular tissue. The invention
 CC also discloses a high throughput method for detecting differentially
 CC expressed cDNAs in a sample. The cDNAs of the invention may have
 CC gynaecological; vasodilator; cytosolic; cardiant; hypotensive; antidiabetic;
 CC antiatherosclerotic; cerebroprotective activities and may be
 CC used in gene therapy. The cDNAs of the invention may be used in a
 CC high-throughput method for detecting differential expression of one or
 CC more cDNAs in a sample or compound that specifically binds a cDNA of the
 CC invention. A protein encoded by the cDNA may be used to screen several
 CC molecules or compounds to identify a ligand that specifically binds to
 CC the protein, or to produce or purify an antibody to the protein that can
 CC be used to detect a protein in a sample or purify a natural or
 CC recombinant protein from a sample. The nucleotides may be useful for
 CC diagnosing, staging, treating, or monitoring the progression of
 CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
 CC artery disease, hypertension, diabetes, pre-eclampsia, ischemia-
 CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used
 CC for large-scale genetic or gene expression analysis of several new
 CC nucleic acid molecules. Antibodies to the proteins encoded by the
 CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic
 CC or acute diseases associated with abnormalities in the expression,
 CC amount or distribution of the protein. The present invention expressed in
 CC activated vascular tissue.
 CC Note: The sequence data for this patent did not form part of the
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov/sequence.html?docID=20020137081>.
 CC
 SQ Sequence 2592 BP; 520 A; 790 C; 766 G; 514 T; 2 other;
 Query Match 97.4%; Score 873.4; DB 25; Length 2592;
 Best Local Similarity 99.7%; Pred. No. 1e-170;
 Matches 896; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 QY 1 ATGACGGAACAGGCGCATCTCTTCCGCAAGACTTCTTGGCCGAGGAGAT-CGCGCGCGC 59
 DB 207 ATGACGGAACAGGCGCATCTCTTCCGCAAGACTTCTTGGCCGAGGAGATCGCGCGCGC 266
 QY 60 CATCTCCAGAGAGGCGCGTGGCTCCGATCGAGC-GGGTCAAGTGTGCTGAGGTCACG 118
 DB 267 CATCTCCAGAGAGGCGCGTGGCTCCGATCGAGCAGCGGGGTCAAGTGTGAGGTCACG 326
 QY 119 ACGCCAGCAAGAGATGCGCGCGGCGAGAGATGACAGGAGGATGCTGACGCTTTC 178
 DB 327 ACGCCAGCAAGAGATGCGCGCGGCGAGAGATGACAGGAGGATGCTGACGCTTTC 386
 QY 179 GCAATCCCAAGAGAGGCGCGTGGCTCTTCTGAGAGGAGGCAACTTCCCAAGTCAATTC 238
 DB 387 GCAATCCCAAGAGAGGCGCGTGGCTCTTCTGAGAGGAGGCAACTTCCCAAGTCAATTC 446
 QY 239 GCTACTTCCCACTCAAGCCTTCAACTTCCGCTTCAAGATATGATGACAGATATCTTC 298
 DB 447 GCTACTTCCCACTCAAGCCTTCAACTTCCGCTTCAAGATATGATGACAGATATCTTC 506
 QY 299 TGGGGGCGTGAACAAGACAGAGTTCGAGAGTACTTTCGGGCAACCTGGCTTCG 358
 DB 507 TGGGGGCGTGAACAAGACAGAGTTCGAGAGTACTTTCGGGCAACCTGGCTTCG 566
 QY 359 GCGGTGCGGCGCGCGAGCTTCCTGCTTGTGATGACCGGCTGATTTTCCAGAACCC 418

Db 567 GCGGTGCGGCGCGCGGACCTCCCTGCTGCTACCCGCTGGATTTCGCAGAACCC 626
QY 419 GCGTGGCAGCGGACGCTGGGAAAAGTCAGCAGACGCGAGTTCGAGCCCTGGAGACT 478
Db 627 GCGTGGCAGCGGACGCTGGGAAAAGTCAGCAGACGCGAGTTCGAGCCCTGGAGACT 686
QY 419 GCGTGGTAAAGTATCAACCAAGTCCGACGGGATCCGGGCGCTGTACCAAGGCTTCAGTGTCT 538
Db 687 GCGTGGTAAAGTATCAACCAAGTCCGACGGGATCCGGGCGCTGTACCAAGGCTTCAGTGTCT 746
QY 539 CCGTGCAGGCGATCATCATCTATCTGCGGCGGCTACTTTCGCGGCTGTACGATACGGGCAAGG 598
Db 747 CCGTGCAGGCGATCATCATCTATCTGCGGCGGCTACTTTCGCGGCTGTACGATACGGGCAAGG 806
QY 599 GCATGCTCCCGCAGCCCAAGAAACAGCAGCATGCTGTAGTGTAGTATGCGGAGACCG 658
Db 807 GCATGCTCCCGCAGCCCAAGAAACAGCAGCATGCTGTAGTGTAGTATGCGGAGACCG 866
QY 659 TGACGCGCGTGGCGCGGCTGTGCTCTACCCCTTGACACAGGTGGCGGCGCATGATGA 718
Db 867 TGACGCGCGTGGCGCGGCTGTGCTCTACCCCTTGACACAGGTGGCGGCGCATGATGA 926
QY 719 TGCAATCCGCGGCGCAAGAGAGCTGACATCATGTACACGGGCGACCGTGCATGTTGGAGGA 778
Db 927 TGCAATCCGCGGCGCAAGAGAGCTGACATCATGTACACGGGCGACCGTGCATGTTGGAGGA 986
QY 779 AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAGGGGTGCGTGTCCAAAGTCTTCC 838
Db 987 AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAGGGGTGCGTGTCCAAAGTCTTCC 1046
QY 839 GGGGCGATGGGGGGCGCTTCTGCTGTGCTCTGTACGAGAGCTCAAGAAAGTGTATCTAA 897
Db 1047 GGGGCGATGGGGGGCGCTTCTGCTGTGCTCTGTACGAGAGCTCAAGAAAGTGTATCTAA 1105

RESULT 7
ACCA6652
ID ACCA6652 standard; cDNA; 2213 BP.
XX
ACCA6652;
XX
02-JUN-2003 (first entry)
XX
DE Human dlthp organelle-associated protein-encoding cDNA.
XX
XX Human; dlthp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW organelle-associated protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US10056.
XX
XX 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX
PA (INCYTE GENOMICS INC.

XX Dafo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;
PI Perilla CH, David MH, Lewis SA, Chen AJ, Penzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RT, Urashka ME;
DR WPI: 2003-129518/12.
DR P-PSDB: ABR41715.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for
PT identifying test compound which specifically binds to a polypeptide
PT encoded by human diagnostic and therapeutic polynucleotide, and to
PT induce antibodies
PS
XX
XX Claim 2; SEQ ID NO 573; 591pp; English.
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dlthp (ACCA6080-ACCA6749) and to their
CC encoded proteins (Dlthp; ABR41136-ABR41812). The invention also relates
CC to polynucleotide sequences at least 90% identical to the dlthp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dlthp nucleic acid sequence; the
CC recombinant production of dlthp proteins; antibodies specific for dlthp
CC proteins; microarrays comprising dlthp nucleic acid sequences; methods
CC of detecting dlthp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a dlthp protein; and methods of
CC assessing the toxicity of test compounds using a dlthp hybridisation
CC probe. Dlthp nucleic acid sequences and dlthp proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. Dlthp
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dlthp nucleic acids are
CC additionally useful in somatic or germ-line gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a dlthp cDNA encoding a dlthp protein
CC which is an organelle-associated protein.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2213 BP; 422 A; 751 C; 633 G; 407 T; 0 other;
Query Match 91.0%; Score 816.4; DB 25; Length 2213;
Best Local Similarity 99.9%; Pred. No. 5,6e-159;
Matches 817; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACGGAACAGGCGCATCTCTTGGCAAAAGCTTGTGGCGAGCATCCGCGCGC 60
Db 206 ATGACGGAACAGGCGCATCTCTTGGCAAAAGCTTGTGGCGAGCATCCGCGCGC 265
QY 61 ATCTCCAAAGCGCGCTGCTCGGATCGAGCGGGTCAACTGCTGTGAGTCCAGCAC 120
Db 266 ATCTCCAAAGCGCGCTGCTCGGATCGAGCGGGTCAACTGCTGTGAGTCCAGCAC 325
QY 121 GCGAGCAACAGATCCCGCCGCAAGAGTCAAGAGGCGATGCTGAGCATGTGCGCGC 180
Db 326 GCGAGCAACAGATCCCGCCGCAAGAGTCAAGAGGCGATGCTGAGCATGTGCGCGC 385
QY 181 ATCCCGAAGAGCGGCGCTGCTCTTGTGAGGGGCAACTTGTCCAAAGTCAATGCGC 240
Db 386 ATCCCGAAGAGCGGCGCTGCTCTTGTGAGGGGCAACTTGTCCAAAGTCAATGCGC 445
QY 241 TACTTCCGACGCAACGCGCTCAACTGCGCTTCAAGAGTAAAGTAAAGAGATCTTCCG 300
Db 446 TACTTCCGACGCAACGCGCTCAACTGCGCTTCAAGAGTAAAGTAAAGAGATCTTCCG 505

Oy		301	GGGCGCCGTGGACAAAGCACAACGCAGTTCCTTGGAAGATCTTTGCGGCAACTGGCCCTCCGGC	369		
Db		506	GCGGCCGTGGACAAAGCACAACGCAGTTCCTTGGAAGATCTTTGCGGCAACTGGCCCTCCGGC	565		
Oy		361	GGTGGCGCCCGCGCGAGACCTCCCTCTGCTGCTGTACACCCTGGATTTTGCAGAACCGC	420		
Db		566	GGTGGCGCCCGCGCGAGACCTCCCTCTGCTGCTGTACACCCTGGATTTTGCAGAACCGC	623		
Oy		421	CTGGCAGCGGACGTGGGAAAGTCCAGCACAGACGCGCATGTTCCGAGCCTGGAGACTGC	480		
Db		626	CTGGCAGCGGACGTGGGAAAGTCCAGCACAGACGCGCATGTTCCGAGCCTGGAGACTGC	685		
Oy		481	CTGTGTAAGAATCACCAAGTCCAGCGGCATCCGGGGCCTGTACACAGGCGCTTCAGTGTCTCC	540		
Db		686	CTGTGTAAGAATCACCAAGTCCAGCGGCATCCGGGGCCTGTACACAGGCGCTTCAGTGTCTCC	743		
Oy		541	GTGCAGGGCATCATCATCTACCGGGCGGCTCTACTTCGGCTGTACGATTCAGGCCAAGGCG	600		
Db		746	GTGCAGGGCATCATCATCTACCGGGCGGCTCTACTTCGGCTGTACGATTCAGGCCAAGGCG	803		
Oy		601	ATGCTCCCCCGACCCCAAAGAACACGCACATCGTGGTAGCTGATGATCCGACAGCCGTG	660		
Db		806	ATGCTCCCCCGACCCCAAAGAACACGCACATCGTGGTAGCTGATGATCCGCGAAGCCGTG	863		
Oy		661	ACGGCCCGTGGCGCCGCGCTGGTGTCTACACCCCTTTCACACAGGCTGGCGCGCATGATATG	720		
Db		866	ACGGCCCGTGGCGCCGCGCTGGTGTCTACACCCCTTTCACACAGGCTGGCGCGCATGATATG	923		
Oy		721	CAGTCTCCGGCGCCAAAGGAGCTGACATCATGTACACCGGGCATCGACTGTTGGAGAGAG	780		
Db		926	CAGTCTCCGGCGCCAAAGGAGCTGACATCATGTACACCGGGCATCGACTGTTGGAGAGAG	985		
Oy		781	ATCTTCACAGATGAGGGGGGCAAGGCGCTTCTTCACAGG	818		
Db		986	ATCTTCACAGATGAGGGGGGCAAGGCGCTTCTTCACAGG	1023		
<hr/>						
RESULT 8						
ID	ABK83761	standard; cdna; 1116 bp.				
AC	ABK83761					
XX	ABK83761:					
DE	14-AUG-2002	(first entry)				
DT	Human cDNA differentially expressed in granulocytic cells #332.					
KW	Human; ss; granulocytic cell; DNA chip; bacterial infection;					
KW	viral infection; parasitic infection; protozoal infection;					
KW	fungal infection; sterile inflammatory disease; psoriasis;					
KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;					
KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;					
KW	adult respiratory distress syndrome; inflammatory bowel disease;					
KW	Crohn's disease; ulcerative colitis; periodontal disease;					
XX	granulocyte activation; chronic inflammation; allergy.					
OS	Homo sapiens.					
PN	M0200228999-AZ.					
PD	11-APR-2002.					
PF	03-OCT-2001; 2001M0-US30821.					
PR	03-OCT-2000; 2000U05-237189P.					
FA	(GENE-) GENE LOGIC INC.					
PI	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;					
RR	WPI; 2002-435328/46.					
XX						

PR Detecting granulocyte activation by detecting differential expression
 PR of genes associated with granulocyte activation, which serves as
 PR diagnostic markers that is useful for monitoring disease states and
 PR drug toxicity -
 XX
 PS Claim 1, SEQ ID No 332; 114pp; English.

Claim 1; SEQ ID No 332; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression (M2) of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g., psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIP0 at http://wipo.int/pub/published_pct_sequences.

SQ Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;

Query Match	Score	DB	Length
86.08;	771.2;	24;	1116;

Matches	786;	Conservative	0;	Mismatches	3;	Indels	3;	Gaps	1;
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Db 1 CTGCAGGTCACGACGCCAGCAAGCAGATCGCCGCCGACACAGCAGTACAAAGGCATCGTG 60

QY 166 GACTGCATTGTCGCGATCCCCAAGGAGCAGGCGTGCTGCTCTTCTGGAGGGCAACCTT 225

Db 61 GACTGCATTGTCGCGATCCCCAAGGAGCAGGGCGTCTGTCTTCTGGAGGGCAACCTT 120

QY 226 GCCAACGTCATTGCTACTTCCCCACTCAAGCCCTCAACTTCGGCTTCAAGGATAAGTAC 285

Db 121 GCCACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCCTCAAGGATAGTAC 180

285 AAGCAGATCTTCTGGGGGGGCGTGGACAAGCACACGCGAGTTCTGGAGGTACTTTGCGGGC 345

Db 181 AAGCAGATCTTCCTGGGGGGCCGTGGACAGACAGACGC---GTTCTGGAGGTACTTTGCGGGC 237

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346 AACCTGGGATCCCGGCCGCACCATCATTTCGTCAACCAGCAAA

A05

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 DB 418 GGCCTCAGTGTCTCCGTGAGGAGGAGATCATCTACCGGGCGCTACTCTCCGCGTGTAC 477
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 DB 658 GACTGTGGAGAGATCTTCAAGATGAGGGGGGCAAGGCTTCTCAAGGGTGTGTG 717
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 DB 718 TCCAAAGTCTGCGGGGCGATGGGGGGCGCTTCTGTGTGTCTGTACGACGACTCAAG 777
 OY 886 AAGGTGATCTAA 897
 DB 778 AAGGTGATCTAA 789
 RESULT 9
 ABN95598
 ID ABN95598 standard; DNA; 1116 BP.
 XX ABN95598;
 AC 13-AUG-2002 (first entry)
 DT Gene #2096 used to diagnose liver cancer.
 DE Gene #2096 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30589.
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI; 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 XX
 PS Claim 1; SEQ ID NO 2096; 298bp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver

CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient. Involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcf_sequences.
 CC
 XX
 SQ Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;
 Query Match 86.0%; Score 771.2; DB 24; Length 1116;
 Best Local Similarity 99.2%; Pred. No. 1e-149; Indels 3; Gaps 1;
 Matches 786; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
 OY 106 CTGCAAGTCCAGCAGCCAGCAGAGATGCGCGCGACACAGTACAAAGGCGATCGT 165
 DB 1 CTGCAAGTCCAGCAGCCAGCAGAGATGCGCGCGACACAGTACAAAGGCGATCGT 60
 OY 166 GACTGCATTTGCCGATCTCCCAAGAGACAGGCGCTGTGTCTTCTGTGAGGGCAACTT 225
 DB 61 GACTGCATTTGCCGATCTCCCAAGAGAGAGGCGCTGTGTCTTCTGTGAGGGCAACTT 120
 OY 226 GCCAAGCTATTCGCTACTTCCCACTCAAGCCCTCAATGCTTCAAGGATTAAGTAC 285
 DB 121 GCCAAGCTATTCGCTACTTCCCACTCAAGCCCTCAATGCTTCAAGGATTAAGTAC 180
 OY 286 AAGCAGATCTTCTGCGGGGCGTGGACAAAGCAGCAGCAGTGTGAGTACTTGTGGGCG 345
 DB 181 AAGCAGATCTTCTGCGGGGCGTGGACAAAGCAGCAGCAGTGTGAGTACTTGTGGGCG 237
 OY 346 AACCTGCGCTCCGCGGCGTGGCGCGGCGGACCTCTCTGTGTGTACCCCGTGTAT 405
 DB 238 AACCTGCGCTCCGCGGCGTGGCGCGGCGGACCTCTCTGTGTGTGTACCCCGTGTAT 297
 OY 406 TTTCGAGAACCCGCGCTGCGACGCGAGCGTGGGAAAGTCAAGAGAGCGGAGTTCCGA 465
 DB 298 TTTCGAGAACCCGCGCTGCGACGCGAGCGTGGGAAAGTCAAGAGAGCGGAGTTCCGA 357
 OY 466 GGCCTGGAGACTGCTCTGGTGAAGATCACCAAGTCCGACGATCCGGGGCCTGTACAG 525
 DB 358 GGCCTGGAGACTGCTCTGGTGAAGATCACCAAGTCCGACGATCCGGGGCCTGTACAG 417
 OY 526 GGCCTCAGTGTCTCCGTGAGGAGGAGATCATCTACCGGGCGCTACTCTCCGCGTGTAC 585
 DB 418 GGCCTCAGTGTCTCCGTGAGGAGGAGATCATCTACCGGGCGCTACTCTCCGCGTGTAC 477
 OY 586 GATACGGCCAAAGGAGGATGCTCCCGACCCCAAGAACACGACATGTGTGTAGCTGTAGT 645
 DB 478 GATACGGCCAAAGGAGGATGCTCCCGACCCCAAGAACACGACATGTGTGTAGCTGTAGT 537
 OY 646 ATCGCGCAGACCGGTGACGGCGCGTGGCGCGTGTGTCTTACCCCTTGACACGGTGTG 705
 DB 538 ATCGCGCAGACCGGTGACGGCGCGTGGCGCGTGTGTCTTACCCCTTGACACGGTGTG 597
 OY 706 CGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
 DB 538 CGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 657
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 DB 658 GACTGTGGAGAGATCTTCAAGATGAGGGGGGCAAGGCTTCTCAAGGGTGTGTG 717
 OY 826 TCCAAAGTCTGCGGGGCGATGGGGGGCGCTTCTGTGTGTCTGTACGACGACTCAAG 885
 DB 718 TCCAAAGTCTGCGGGGCGATGGGGGGCGCTTCTGTGTGTCTGTACGACGACTCAAG 777
 OY 886 AAGGTGATCTAA 897

DB 778 AAGTGATCTAA 789

RESULT 10
ABL69347
ID ABL69347 standard; DNA: 1116 BP.

AC ABL69347;

XX 15-MAY-2002 (first entry)

XX Prostate cancer related gene sequence SEQ ID NO:7684.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.

OS Homo sapiens.

PN WO200194629-A2.

DD 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-208473P.

XX 18-SEP-2000; 2000US-235133P.

XX 20-SEP-2000; 2000US-234034P.

XX 22-SEP-2000; 2000US-234509P.

XX 25-SEP-2000; 2000US-234567P.

XX 25-SEP-2000; 2000US-234923P.

XX 25-SEP-2000; 2000US-235077P.

XX 25-SEP-2000; 2000US-235134P.

XX 25-SEP-2000; 2000US-235280P.

XX 26-SEP-2000; 2000US-235637P.

XX 27-SEP-2000; 2000US-235711P.

XX 27-SEP-2000; 2000US-235840P.

XX 28-SEP-2000; 2000US-236028P.

XX 28-SEP-2000; 2000US-236032P.

XX 28-SEP-2000; 2000US-236033P.

XX 28-SEP-2000; 2000US-236034P.

XX 28-SEP-2000; 2000US-236109P.

XX 28-SEP-2000; 2000US-236113P.

XX 29-SEP-2000; 2000US-236842P.

XX 29-SEP-2000; 2000US-236891P.

XX 02-OCT-2000; 2000US-237117P.

XX 02-OCT-2000; 2000US-237173P.

XX 02-OCT-2000; 2000US-237294P.

XX 02-OCT-2000; 2000US-237295P.

XX 02-OCT-2000; 2000US-237316P.

XX 03-OCT-2000; 2000US-237425P.

XX 03-OCT-2000; 2000US-237598P.

XX 03-OCT-2000; 2000US-237604P.

XX 03-OCT-2000; 2000US-237606P.

XX 03-OCT-2000; 2000US-237608P.

XX 01-NOV-2000; 2000US-244867P.

XX 01-NOV-2000; 2000US-245084P.

XX (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a

XX chemical agent to be tested for anti-neoplastic activity, and

XX determining a change in expression of a gene of a signature gene set

XX Claim 1; SEQ ID 7684; 44pp: English.

XX The present invention describes a method (M1) for screening for an
XX anti-neoplastic agent. The method involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (1) of a signature gene set, where (1)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61864
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (1) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening
XX an anti-neoplastic agent, and can be used for producing a product which
XX is the data collected with respect to the anti-neoplastic agent as a
XX result of M1, and the data is sufficient to convey the chemical
XX structure and/or properties of the agent. M1 can be used in the
XX treatment of cancer such as colon, breast, stomach, lung, thyroid,
XX oesophageal, ovarian, kidney, prostate or pancreatic cancer,
XX adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
XX infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
XX carcinoma, papillary carcinoma and Wilm's tumour.

XX Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other:

XX Query Match 86.0%; Score 771.2; DB 24; Length 1116;
XX Best Local Similarity 99.2%; Pred. No. 1e-149; 3; Indels 3; Gaps 1;
XX Matches 786; Conservative 0; Mismatches 3;

XX 106 CTGACGCTCAGCAGCCAGCAAGCATGCGCGGAGCAAGCATCAAGGAGTCAAGGAGTGGT 165

XX 1 GATGAGTTCAGCAGCCAGCAAGCATGCGCGGAGCAAGCATCAAGGAGTCAAGGAGTGGT 60

XX 166 GACTGATGTCGCGATCCCAAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 225

XX 61 GACTGATGTCGCGATCCCAAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120

XX 226 GCCAGGTCATTCGCTACTTCCCAAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 285

XX 121 GCCAGGTCATTCGCTACTTCCCAAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180

XX 286 AAGCAGATCTTCCTGGGGGGGGTGGAGCAAGCAGCAGTTCGAGTACTTGGCGGC 345

XX 181 AAGCAGATCTTCCTGGGGGGGGTGGAGCAAGCAGCAGTTCGAGTACTTGGCGGC 237

XX 346 AACCTGGCTCCGGGGGGTGGAGCAAGCAGCAGTTCGAGTACTTGGCGGC 405

XX 238 AACCTGGCTCCGGGGGGTGGAGCAAGCAGCAGTTCGAGTACTTGGCGGC 297

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XX 526 GGGTTCAGTGTCTCGTGGAGGATCATATCTACCGGGGGGCTACTTGGGGGTGAC 585

XX 418 GGGTTCAGTGTCTCGTGGAGGATCATATCTACCGGGGGGCTACTTGGGGGTGAC 477

XX 586 GATACGGCCAAAGGCAATGCTCCCGAGCCCAAGCAAGCAGCATGCTGGTGAAGTGCATG 645

XX 478 GATACGGCCAAAGGCAATGCTCCCGAGCCCAAGCAAGCAGCATGCTGGTGAAGTGCATG 537

XX 646 ATCCGCGAGACCGTGAAGCGCCGTGGCGGCGGTGTCTACCCCTTCGACAGCGTGGC 705

XX 538 ATCCGCGAGACCGTGAAGCGCCGTGGCGGCGGTGTCTACCCCTTCGACAGCGTGGC 597

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 01:25:37 ; Search time 2414 Seconds

(without alignments)
9031.116 Million cell updates/sec

Title: US-09-811-094-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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18: em_gss_huv:*
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21: em_gss_fun:*
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28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	895.4	99.8	1355	11	BC035469 Homo sapi
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5	848	94.5	1201	9	AL534908
6	838.4	93.5	949	13	BQ932832
7	837.6	93.4	922	13	BQ226117
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9	829.8	92.5	1201	9	AL539376
10	821.4	91.6	1201	9	AL557414
11	821	91.5	1201	9	AL514420
12	815.2	90.9	1071	12	BM554606
13	813.8	90.7	1014	13	BX375536
14	810.8	90.4	931	13	BQ933670
15	808.6	90.1	1201	13	BX423613
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20	799.8	89.2	955	13	BQ677977
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24	791.6	88.2	836	12	BI084258
25	790.6	88.1	951	13	BQ528404
26	789.8	88.0	1055	13	BX415427
27	789.6	88.0	1184	9	AL527028
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38	775.4	86.4	989	12	BM471365
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40	772.6	86.1	1017	12	BM608760
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ALIGNMENTS

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ACCESSION BC013256
VERSION BC013256.1 GI:15301544
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 1355)
JOURNAL Direct Submission
Submitted (27-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (TMCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villalobdbcm.tmc.edu.
 Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 13 Row: e Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA g1: 3820534
 This clone has the following problem: no 5' EST match.

FEATURES

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 /tissue_type="Eye, retinoblastoma"
 /clone_lib="NIH_MGC_67"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"

BASE COUNT 283 a 417 c 404 g 251 t

ORIGIN

Query Match 99.8%; Score 895.4; DB 11; Length 1355;
 Best Local Similarity 99.9%; Pred. No. 8,4e-183;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 ATGACGAGACAGGCGATCTCTCTCGCAAGACTTCTGGCGGAGAGCATCGCGCGCC 60
 92 ATGACGAGACAGGCGATCTCTCTCGCAAGACTTCTGGCGGAGAGCATCGCGCGCC 151
 61 ATCTCCAGAGCGCGCGCTCGAGAGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTC 120
 152 ATCTCCAGAGCGCGCGCTCGAGAGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTC 211
 121 GCGACAGAGAGAGCGCGCGCGCGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAG 180
 212 GCGACAGAGAGAGAGCGCGCGCGCGAGAGAGTCAAGAGAGAGAGAGAGAGAGAG 271
 181 ATCCCAAG 240
 272 ATCCCAAG 331
 241 TACTTCCCACTCAAGCGCTCACTTCCGCTTCAAGAGATAGTACAGAGAGATCTTCG 300
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 DB 872 ATCTCCAG 931
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RESULT 2
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 LOCUS
 DIRECT REPEAT
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (Mammalia) to 1355)
 Strausberg R
 Direct Submission
 Submitted (31-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC) Cancer Genomics Office, National Cancer
 Institute, 31 Center drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT
 NHI-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: g9apds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.M., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 13 Row: f Column: 9
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA g1: 4503556
 This clone has the following problem: no 5' EST match.

FEATURES

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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="3867130"
 /tissue_type="Eye, retinoblastoma"
 /clone_lib="NIH_MGC_67"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"

BASE COUNT 283 a 417 c 404 g 251 t

ORIGIN

Query Match 99.8%; Score 895.4; DB 11; Length 1355;
 Best Local Similarity 99.9%; Pred. No. 8,4e-183;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 212 GCCAGCAAGCAGATGCGCCGCGACAAAGAGTACAAAGGCGATGTCATCTTCTCCG 271
QY 181 ATCCCAAGAGGAGGAGGCGCTGCTGTCTTCTTGAGGCGCAACCTTCCAAAGTATGCG 240
DB 272 ATCCCAAGAGGAGGAGGCGCTGCTGTCTTCTTGAGGCGCAACCTTCCAAAGTATGCG 311
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DB 392 GGGGCGGTGGAGACACAGCAGATCTGAGAGTACTTTCGCGGCAACCTGGCCCTCCG 451
QY 361 GGTGGGCGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 452 GGTGGGCGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 511
QY 421 CTGGCAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTCCGAGGCGCTGGGAGACTGC 480
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LOCUS BX419742 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CSDF020YC16 5-PRIME, mRNA sequence.
ACCESSION BX419742
VERSION BX419742.1 GI:30642547
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
```

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REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDF020B08Q1&cluster=10389.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSDF020B08Q1.

FEATURES
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/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: Brain; Vector: pCMVSPORT.6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 245 a 365 c 354 g 210 t 27 others
ORIGIN
Query Match 95.7%; Score 858.4; DB 13; Length 1201;
Best Local Similarity 97.8%; Pred. NO. 7.6e-175;
Matches 878; Conservative 11; Mismatches 7; Indels 2; Gaps 2;

QY 1 ATGACGGAACAGCCATCTCTTCCGCAAAAGCTTCTTGCGGAGGACATCCGCCGCC 60
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DB 272 GCCAGCAAGCAGATGCGCCGCGACAAAGAGTACAAAGGCGATGTCATCTTCTCCG 331
QY 181 ATCCCAAGAGGAGGAGGCGCTGCTGTCTTCTTGAGGCGCAACCTTCCAAAGTATGCG 240
DB 332 ATCCCAAGAGGAGGAGGCGCTGCTGTCTTCTTGAGGCGCAACCTTCCAAAGTATGCG 391
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DB 452 GGGGCGGTGGAGACACAGCAGTCTGAGAGTACTTTCGCGGCAACCTGGCCCTCCG 511
QY 361 GGTGGGCGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 512 GGTGGGCGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 571
QY 421 CTGGCAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTCCGAGGCGCTGGGAGACTGC 480
DB 572 CTGGCAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTCCGAGGCGCTGGGAGACTGC 631
QY 481 CTGGTGAAGATCAACCAAGTCCGACGCGATCCGCGGCGCTGTACAGGCGCTTCAAGTCTCC 540
DB 632 CTGGTGAAGATCAACCAAGTCCGACGCGATCCGCGGCGCTGTACAGGCGCTTCAAGTCTCC 691
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QY	600	CATCTCTCCCGACCCCAAGAACAGCGCATCTCGTGGTGAAGTATGATCCGAGACCGT		659
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QY	660	GACGGCCGCTGGCGCGGTGTCCTTACCCCTTCAGACAGGTGGGGGGCGATATGAT		719
Db	812	GACGGCCGCTGGCGCGGTGTCCTTACCCCTTCAGACAGGTGGGGGGCGATATGAT		871
QY	720	GCACTCCGGGGCGAAGAGAGCTGACATCATGTATACAGGGGACCGTCGATCTGTGGAGGAA		779
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QY	840	GGGCATGTGGGGGGCGCTTGTGTCTGTGGTCTGTACGACGAGCTCAAGAGGTGATCTTAA		897
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RESULT 4	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AL545701		1201 bp mRNA linear	AL545701			Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		Li, W.B., Gruber, C., Jesse, J., and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished	On Feb 15, 2001, this sequence version replaced g1:12878183.
		clone CSOD1009H03 5'-PRIME, mRNA sequence.	AL545701									
			AL545701.2	GI:31267536	EST							

Contact: genoscope
genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389_r For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI009CD020P1cluster=10389_r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI009CD020P1cluster=10389_r). Contact :
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue genoscope.sequence ID : CS0DI009CD020P1.

FEATURES	location/qualifiers
source	1. .1201

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/notes="1st strand cDNA was primed with a NotI primer. Five prime end enriched, double-stranded digested with Not I and cloned into the Not I sites of the pCMVSPORT 6 vector. Library was r
248 a 362 c 372 g 218 t 1 others
BASE COUNT
ORIGIN

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Query Match	94.88;	Score 850.8;	DB 9;	Length 1201;
Best Local Similarity	98.88;	Pred. No. 3.3e-173;		
Matches 878; Conservative	0;	Mismatches 8;	Indels 3;	Gaps 2

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Db	58	ATGCATCTCTCTTGGCAAAAGACTTTTGGCCGGAGAGCATATGCCGCCATCTCCMAA	117
QY	71	CGGCGTGGGCTCGATCGAGCGGGTCAAAGCTGCTGTGAGGTCCAGACGCCAGCAAGC	130
Db	118	CGGCGTGGGCTCGATCGAGCGGGTCAAAGCTGCTGTGAGGTCCAGACGCCAGCAAGC	177
QY	131	AGATGGCGCGCGCAAGACAGTCAAAAGGACATCTGTGACATCTATTGTCCGATCCCAAG	190
Db	178	AGATGGCGCGCGCAAGACAGTCAAAAGGACATCTGTGACATCTATTGTCCGATCCCAAG	237
QY	191	AGCAGGGCGTGTCTCTTCTGAGAGGGCAACCTTCGCMAACATCTACCTTCCCA	250
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QY	251	CTCAAGGCCCTCACTCTCGGCTTCAAGAGTAAGTACAAGACATCTTCTCTGGGGGGCTGTG	310
Db	298	CTCAAGGCCCTCACTCTCGGCTTCAAGAGTAAGTACAAGACATCTTCTCTGGGGGGGGTGTG	357
QY	311	ACAAGCACACGAGTCTTGAGAGTACTTGGGGGCAACCTGGCCTCCGCGGATGCGGCGG	370
Db	358	ACAAGCACACGAGTCTTGAGAGTACTTGGGGGCAACCTGGCCTCCGCGGATGCGGCGG	417
QY	371	GGCGAGCTCCCTCTCTCTGTGTACCCGCTGGATTTTCCAGAAACCCGCTGGACAGCG	430
Db	418	GGCGAGCTCCCTCTCTCTGTGTACCCGCTGGATTTTCCAGAAACCCGCTGGACAGCG	477
QY	431	ACGCTGGAAAGTAGGACACAGAGCCGAGTTCGAGGAGCTGGAGAGTACCTGGTGAAG	490

Db 478 AGCTGGGAAGTACAGGCACAGAGCCGAGTCTCCAGAGCCTGGGAACACTGCTGGTGAACA 537

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Db 538 TCACCAAACTCGACAGGCATCTCCGGGGCCTGTACAGGGCTTCAAGTGTCTCCCTGCAGAGCA 597

QY 551 TCATCATCTAACGGGGGGGCTACTTCCGCGGTGTACGATACGGCCAAAGGGCATGTCTCCCG 610

Db 598 TCATCATCTAACGGGGGGGCTACTTCCGCGGTGTACGATACGGCCAAAGGGCATGTCTCCCG 657

QY 611 ACCCCCAAAACAGCAACATCTGTGTAGACTGGATGATACGGCAGACCTGTACGGCCGTGG 670

Db 658 ACCCCCAAAACAGCAACATCTGTGTAGACTGGATGATACGGCAGACCTGTACGGCCGTGG 717

QY 671 CCGGGGTGTGTCTCTTACCCCTTCGACAGGGTGGCGGGCCATGATGTGAGTGCAGTCCGGG 730

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Db 897 GGGCGCTTCTGTGTGTCTGTATGAGAGAGACTCAAAAGGTATCTAA 945

RESULT 5	AL534908	1201 bp	linear	EST 12-MAY-2001
LOCUS	AL534908			
DEFINITION	AL534908 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone			
ACCESSION	CSDD0007120 5-PRIME, mRNA sequence.			
VERSION	AL534908			
	AL534908.2 GI:30541165			

KEYWORDS EST.
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Query Match 93.5%; Score 838.4; DB 13; Length 949;
Best Local Similarity 97.8%; Pred. No. 1.5e-170;
Matches 870; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 1 ATGACGAAACAGGCGATCTCTTCCGCAAAAGCTTTCTGGCCGAGAGCATCCGCCGCC 60
DB 1 ATGACGAAACAGGCGATCTCTTCCGCAAAAGCTTTCTGGCCGAGAGCATCCGCCGCC 112
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QY 121 GCCAGCAAGAGATGCGCGCGCGCAAGAGGAGGATCGTGACATGTCATGTCGCC 180
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DB 713 AGCG 772
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DB 773 CAGTCGCGCGCGCGAG 832
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LOCUS AGENCOURT.7576905 NIH_MGC_68 Homo sapiens cDNA IMAGE:6058842
DEFINITION 5' mRNA sequence.
ACCESSION BO226117.1 GI:20407526
VERSION
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 922)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13324 row: 1 column: 19
High quality sequence stop: 317.
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Average insert size 1.8 kb. Library constructed by Life
Technologies".
BASE COUNT 184 a 296 c 280 g 162 t
ORIGIN

Query Match 93.4%; Score 837.6; DB 13; Length 922;
Best Local Similarity 96.7%; Pred. No. 2.2e-170;
Matches 866; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 1 ATGACGAAACAGGCGATCTCTTCCGCAAAAGCTTTCTGGCCGAGAGCATCCGCCGCC 60
DB 26 ATGACGAAACAGGCGATCTCTTCCGCAAAAGCTTTCTGGCCGAGAGCATCCGCCGCC 84
QY 61 ATTCGCAAGAGGCGCGTGGCTCCGATCGAGGGGTCAAGTGTGTGAGGTCCAGAC 120
DB 85 ATTCGCAAGAGGCGCGTGGCTCCGATCGAGGGGTCAAGTGTGTGAGGTCCAGAC 144
QY 121 GCCAGCAAGAGATGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 145 GCCAGCAAGAGATGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 204
QY 181 ATCCGCAAGAGAGAGGAGGTGTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 205 ATCCGCAAGAGAGAGGAGGTGTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 284
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DB 265 TACTTCCCACTCAAGCCCTCAATTCGCTTCAAGGATTAAGTACAAGCATCTTCTCG 324
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RESULT 8
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DEFINITION CS0DF032YN01 5-PRIME, mRNA sequence.
ACCESSION AL540267
VERSION AL540267.2 GI:31264828
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1201)
JOURNAL Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
COMMENT On Feb 15, 2001 this sequence version replaced gi:12870254.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10389.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF032CG01Q1&cluster=10389.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF032CG01Q1.

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/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

BASE COUNT 249 a 349 c 357 g 218 t 28 others
ORIGIN

Query Match 93.2%; Score 836.2; DB 9; Length 1201;
Best Local Similarity 99.2%; Pred. No. 4, 6e-170;
Matches 860; Conservative 1; Mismatches 4; Indels 2; Gaps 2;

QY 1 ATGACGGAACAGGCGGCTTCTGCGCAAGAGCTTGTGGCGGAGCATCGCGCGCGC 60
Db 159 ATGACGGAACAGGCGGCTTCTGCGCAAGAGCTTGTGGCGGAGG-ATCGCGCGCGC 217
QY 61 ATCTCCAAAGAGCGGCGTGGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGGTCCAGC 120
Db 218 ATCTCCAAAGAGCGGCGTGGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGGTCCAGC 277
QY 121 GCCAGCAAGCAGATGCGCGCGCGAGCAAGAGTACAGAGCGATCGTGTATGTCTCGC 180
Db 278 GCCAGCAAGCAGATGCGCGCGCGAGCAAGAGTACAGAGCGATCGTGTATGTCTCGC 337
QY 181 ATCCCAAGAGAGGAGGCGGCTGCTGCTTGTGAGGAGGCAACCTTCCAAAGCATCTCC 240
Db 338 ATCCCAAGAGAGGAGGCGGCTGCTGCTTGTGAGGAGGCAACCTTCCAAAGCATCTCC 397
QY 241 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGATTAAGTACAGAGATCTTCTCG 300
Db 398 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGATTAAGTACAGAGATCTTCTCG 457
QY 301 GGGGCGGTGAGACAGCAGCAGAGTCTGTGAGTACTTGTGCGGCAACTGCGCTCGCG 360
Db 458 GGGGCGGTGAGACAGCAGCAGAGTCTGTGAGTACTTGTGCGGCAACTGCGCTCGCG 517
QY 361 GGTGGGCGGCGGCGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 518 GGTGGGCGGCGGCGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 577
QY 421 CTGGCAGCGGAGCTGTGGGAAAGTCAAGAGCAGAGCGGAGTTCGAGCGCTGGAGACTCG 480
Db 578 CTGGCAGCGGAGCTGTGGGAAAGTCAAGAGCAGAGCGGAGTTCGAGCGCTGGAGACTCG 637
QY 481 CTGGTCAAGATCAACCAAGTCCGAGCGCATCCGGGCGCTGTACAGAGGCTTCAAGTCTCC 540
Db 638 CTGGTCAAGATCAACCAAGTCCGAGCGCATCCGGGCGCTGTACAGAGGCTTCAAGTCTCC 697
QY 541 GTGCAAGGCAATCATCTATCCAGCGGCGGCTTACTTGGGCGTGTACATACGCGCAAGGCG 600
Db 698 GTGCAAGGCAATCATCTATCCAGCGGCGGCTTACTTGGGCGTGTACATACGCGCAAGGCG 757
QY 601 ATGCTCCCGGACCCCAAGAACAGCAGCATCTGTGTAGTGTGATTCGCGAGACCGTG 660
Db 758 ATGCTCCCGGACCCCAAGAACAGCAGCATCTGTGTAGTGTGATTCGCGAGACCGTG 817
QY 661 ACAGCGGTGGCGGCGTGTGTCTTACCCCTTGCACAGCGGTGGCGGCGCATGATGATG 720
Db 818 ACAGCGGTGGCGGCGTGTGTCTTACCCCTTGCACAGCGGTGGCGGCGCATGATGATG 877
QY 721 CAGTCCGCGGCGCAAGAGAGTGCATCATGTACAGCGGCGCATGCTGCAAGTGTGGAAG 780
Db 878 CAGTCCGCGGCGCAAGAGAGTGCATCATGTACAGCGGCGCATGCTGCAAGTGTGGAAG 937
QY 781 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGCTGCTGTCCAAAGTCTGCGG 840
Db 938 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGCTGCTGTCCAAAGTCTGCGG 997
QY 841 GGCATGCGGGGCGGCGCTTCTGCTGTGTC 867
Db 998 GGCATGCGGGGCGGCGCTTCTGCTGTGTC 1023

RESULT 9
AL539376 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL539376 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF033Y01 5-PRIME, mRNA sequence.
ACCESSION AL539376
VERSION AL539376.2 GI:31263944
EST.

SOURCE ORGANISM	REFERENCE
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 1201)	
Li, W. B., Gruber, C., Jesssee, J. and Polayes, D.	
Full-length cDNA libraries and normalization	
Unpublished	
On Feb 15, 2001 this sequence version replaced gi:12868534.	

FEATURES

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Mitsubishi. This sequence belongs to sequence cluster 10389_r For
more information about this cluster, see
<http://www.genoscope.cns.fr/cluster>, see
http://www.genoscope.cns.fr/cluster-10389_r. Contact :
Feng Liang Email: liang@life.com/invitrogen.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF033MH10QPI.
Location/Qualifiers

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1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDF033YO19"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_1b="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: PCMVSPORT_6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized."
358 c 360 g 221 t 20 others
242 a

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ORIGIN	Query Match	Score	DB	Length
	92.58;	829.8;	9;	1201;

[illegible]

QY	481	CTGGGAAATGATCAAGTCGAGGGCATCCGGGCGCTGTACACAGGCGTTAGTGTCTCC	540
Db	637	CTGGTGAAGATCAACAAGTCGACCGGATCCGGGCGCTGTACACAGGCGTTAGTGTCTCC	696
QY	541	GTGCAAGGCATCATCATCTATCAACGGGGGGCGCTACATCGGGCTGTACAGATACGGCCAAAGGC	600
Db	697	GTGCAAGGCATCATCATCTATCAACGGGGGGCGCTACTTGGCGCTGTACAGATACGGCCAAAGGC	756
QY	601	ATGCTCTCCCGACCCCAAGAAACACGACATCGTGTGATGCTGATATGTCGCCAACCGTG	660
Db	757	ATGCTCTCCCGACCCCAAGAAACACGACATCGTGTGATGCTGATATGTCGCCAACCGTG	816
QY	661	ACGGCGCTGGCGCGGGTGGTGTCTCAACCCCTTGACACAGGTGCGCGCGGCGCATGTATGATG	720
Db	817	ACGGCGCTGGCGCGGGTGGTGTCTCAACCCCTTGACACAGGTGCGCGCGGCGCATGTATGATG	874
QY	721	CAGTTCGGGCGCAAGAGAACCTGACATCATGTATACACGGGCACCGTGCAGCTGT - GGAAGAA	779
Db	875	CAGTTCGGGCGCAAGAGAACCTGACATCATGTATACACGGGCACCGTGCAGCTGTGGAAGAA	934
QY	780	GATCTTCAGAGATGA - GGGGGGCAAGGCGCTTCTTCAAGAGGTGCGGTCCACAGCTCTGCG	838
Db	935	GATCTTCAGAGATGAAGGGGGGCAAGGCGCTTCTTCAAGAGGTGCGGTCCACAGCTCTGCG	994
QY	839	GGGGCATAGGGGGCGCGCTTCTGTGTGTGCTCTGTACGACAGGCTCAAGAGGTGATCTTAA	897
Db	995	GGGGCATAGGGGGCGCGCTTCTGTGTGTGCTCTGTGTGACGAGGCTCAAGAGAGGTGATCTTAA	1053

RESULT 10	LOCUS	DEFINITION	VERSION
AL557414	1201 bp	linear	EST 31-MAY-2000
AL557414	Homo sapiens T CELLS (JURKAT CELL LINE)	Homo sapiens cDNA	
AL557414	clone CS0DH003YD19 5-PRIME	mRNA sequence	
AL557414.2	GI:31279214		

KEYWORDS	EST.
ORGANISM	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ATTNRS	1 (bases 1 to 1201)
TTLE	L.I.W.B., Gruber,C., Jesse,J., and Polayes,D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12900994.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, **Web :** www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 10389.r For more information about this cluster, see
[http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DH003CB10QP1&cluster=10389.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DH003CB10QP1&cluster=10389.r). **Contact :**
 Feng Liang Email : liang@lifetech.com **URL :**
<http://www.length.invitrogen.com/Invitrogen>
 Faraday Avenue Genoscope sequence ID : CS0DH003CB10QP1.
 location/Qualifiers
 1. 1201

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDBH003YD19"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/notes="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

```

BASE COUNT 239 a 358 c 348 g 222 t 34 others
 ORIGIN

Query Match
 Best Local Similarity 91.6%; Score 821.4; DB 9; Length 1201;
 Matches 877; Conservative 6; Mismatches 7; Indels 5; Gaps 5;

1 ATGACGGAACAGGCCATCTCTCTGCGCAAGACTCTTGGCCGAGGATCGCCGCC 60
 |||||
 138 ATGACGGAACAGGCCATCTCTCTGCGCAAGACTCTTGGCCGAGGATCGCCGCC 196
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61 ATCTCCAAAGAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCACAC 120
 |||||
 197 ATCTCCAAAGAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCACAC 256
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121 GCCAGCAGCAGATCTGCGCGCGCAAGAGTCAAGAGGATCTGTGACTGTCACCG 180
 |||||
 257 GCCAGCAGCAGATCTGCGCGCGCAAGAGGATCTGTGACTGTCACCG 316
 |||||

181 ATCCCAAGAGCAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 240
 |||||
 317 ATCCCAAGAGCAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 376
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241 TACTTCCCACTCAAGCGCTCAACTCTGCTTCAAGGATTAAGTCAAGCAGATCTCTG 300
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 377 TACTTCCCACTCAAGCGCTCAACTCTGCTTCAAGGATTAAGTCAAGCAGATCTCTG 436
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301 GGGGGCGTGGACAGCAGCAGAGTCTGAGAGTACTTGGCGCAACCTGGCCCTCGGC 360
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 437 GGGGGCGTGGACAGCAGCAGAGTCTGAGAGTACTTGGCGCAACCTGGCCCTCGGC 496
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361 GGTGGCGCGCGCGCAGCTCTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 420
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 497 GGTGGCGCGCGCGCAGCTCTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 556
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421 CTGGCAGCGGAGCTGGGAAAGTCAAGCAGCAGAGTCTGAGCGCTGGAGCGCTGAGACTGC 480
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 557 CTGGCAGCGGAGCTGGGAAAGTCAAGCAGCAGAGTCTGAGCGCTGGAGCGCTGAGACTGC 616
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481 CTGGTGAAGATCAACAGCTCCGAGCGCATCCGGCGCTGACAGGCGCTCACTGTCTCC 540
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 617 CTGGTGAAGATCAACAGCTCCGAGCGCATCCGGCGCTGACAGGCGCTCACTGTCTCC 676
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541 GTTCAGGCGCATCATCTACCGCGCGCTTACTTGGCGCTGATCAAGTCAAGCGCAAGGCG 600
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 677 GTTCAGGCGCATCATCTACCGCGCGCTTACTTGGCGCTGATCAAGTCAAGCGCAAGGCG 736
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601 ATGCTCCCGAGCGCGCAAGAGCAGCAGATCTGTGAGTGAATGATCGCGCAGACCGTGC 660
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 737 ATGCTCCCGAGCGCGCAAGAGCAGCAGATCTGTGAGTGAATGATCGCGCAGACCGTGC 796
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661 ACAGCGGTGCGCGCGT - GGTGTCTACCTCTGACACAGCGTGGCGCGCATG - ATGA 718
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 797 ACAGCGGTGCGCGCGTGGGTGTCTACCTCTGACACAGCGTGGCGCGCATGATGA 856
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719 TCGATGTCGGGGCGCAAGAGCTGACATCATGTACACAGGCGCATCTGTGAGGA 778
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 857 TCGATGTCGGGGCGCAAGAGCTGACATCATGTACACAGGCGCATCTGTGAGGA 916
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779 AGATCTTCAAGATGAGGGGGGAGGCGCTTCTTCAAGGAGTGTGCTGATCAAGTCTGC 838
 |||||
 917 AGATCTTCAAGATGAGGGGGGAGGCGCTTCTTCAAGGAGTGTGCTGATCAAGTCTGC 975
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839 GGGGCGTGGGGCGCGCTTCTGCTGATCTGATCAAGCAGCAGTCAAGAGTGTAT 893
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 976 GGGGCGTGGGGCGCGCTTCTGCTGATCTGATCAAGCAGCAGTCAAGAGTGTAT 1029
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RESULT 11
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 LOCUS AL514420 Homo sapiens NEUROBLASTOMA
 DEFINITION CL0BB0102F01 5-PRIME, mRNA sequence.

ACCESSION AL514420
 VERSION AL514420.2
 KEYWORDS GI:30464305
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 1 (bases 1 to 1201)
 Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 unpublished

COMMENT
 On Feb 13, 2001 this sequence version replaced gi:12777914.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10389.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CL0BB0102F01R1&cluster=10389.r. Contact :
 Feng Liang Email : fliang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CL0BB0102F01R1.
 Location/Qualifiers
 1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CL0BB0102F01"
 /issue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: pCMVSPORT.6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT 233 a 346 c 370 g 219 t 33 others
 ORIGIN

Query Match
 Best Local Similarity 91.5%; Score 821; DB 9; Length 1201;
 Matches 849; Conservative 7; Mismatches 17; Indels 2; Gaps 2;

1 ATGACGGAACAGGCCATCTCTCTGCGCAAGACTCTTGGCCGAGGATCGCCGCC 60
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 129 ATGACGGAACAGGCCATCTCTCTGCGCAAGACTCTTGGCCGAGGATCGCCGCC 187
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61 ATCTCCAAAGAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 120
 |||||
 188 ATCTCCAAAGAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 247
 |||||

121 GCCAGCAGCAGATCTGCGCGCGCAAGAGTCAAGAGGATCTGTGACTGTCACCG 180
 |||||
 248 GCCAGCAGCAGATCTGCGCGCGCAAGAGTCAAGAGGATCTGTGACTGTCACCG 307
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181 ATCCCAAGAGCAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 240
 |||||
 308 ATCCCAAGAGCAGCGCGTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 367
 |||||

241 TACTTCCCACTCAAGCGCTCAACTCTGCTTCAAGGATTAAGTCAAGCAGATCTCTG 300
 |||||
 368 TACTTCCCACTCAAGCGCTCAACTCTGCTTCAAGGATTAAGTCAAGCAGATCTCTG 427
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301 GGGGGCGTGGACAGCAGCAGAGTCTGAGAGTACTTGGCGCAACCTGGCCCTCGGC 360
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 428 GGGGGCGTGGACAGCAGCAGAGTCTGAGAGTACTTGGCGCAACCTGGCCCTCGGC 487
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361 GGTGGCGCGCGCGCAGCTCTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 420
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 488 GGTGGCGCGCGCGCAGCTCTCTGCTGATCGAGCGGCTGAAGTGTGTGACAGGTCAC 547
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421 CTGGCAGCGGAGCTGGGAAAGTCAAGCAGCAGAGTCTGAGCGCTGGAGCGTGC 480
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ACCESSION BX375536
 VERSION BX375536.1 GI:30456413
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1014)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r for more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC014BD12Q1&cluster=10389.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC014BD12Q1.
 FEATURES
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 1..1014
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC014YG24"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 192 a 317 c 318 g 185 t 2 others
 ORIGIN
 Query Match 90.7%; Score 813.8; DB 13; Length 1014;
 Best local Similarity 98.9%; Pred. No. 3e-165;
 Matches 848; Conservative 2; Mismatches 4; Indels 3; Gaps 3;
 QY 1 ATGAGGAGACAGGCGCTCTCTGCGCAAGAGATTCTTGGCGGAGGCGATCGCGCGC 60
 DB 159 ATGAGGAGACAGGCGCTCTCTGCGCAAGAGATTCTTGGCGGAGGCGATCGCGCGC 217
 QY 61 ATCTCCAGAGCGCGCTGCTCCGATCGAGCGGGGTGAAGTGTGCTGCGAGTCCAGCAC 120
 DB 218 ATCTCCAGAGCGCGCTGCTCCGATCGAGCGGGGTGAAGTGTGCTGCGAGTCCAGCAC 277
 QY 121 GCCAGCAGCAGATCGCGCGCGCAAGAGTACAGAGGCGATCGTGCATTTGTCGCG 180
 DB 278 GCCAGCAGCAGATCGCGCGCGCGCAAGAGTACAGAGGCGATCGTGCATTTGTCGCG 337
 QY 181 ATCCCAAGAGAGGCGGTGCTCTTCTGAGGGGCAACTTGCACAAGTCAATTCGC 240
 DB 338 ATCCCAAGAGAGGCGGTGCTCTTCTGAGGGGCAACTTGCACAAGTCAATTCGC 397
 QY 241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGGATTAAGTACAAGAGATCTTCG 300
 DB 398 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGGATTAAGTACAAGAGATCTTCG 457
 QY 301 GGGGGCGGTGAGACAGCAGAGTCTGAGAGTACTTTGCGGCAACTGCGCTCGGC 360
 DB 458 GGGGGCGGTGAGACAGCAGAGTCTGAGAGTACTTTGCGGCAACTGCGCTCGGC 517
 QY 361 GGTGGCGCGCGCGCGACCTCTCTGCTTGTACCCGCTGGATTTTGGCAGACCCGC 420
 DB 518 GGTGGCGCGCGCGCGACCTCTCTGCTTGTACCCGCTGGATTTTGGCAGACCCGC 577
 QY 421 CTGGAGCGGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCCGAGGCGCTGGAGACTGC 480
 DB 578 CTGGAGCGGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCCGAGGCGCTGGAGACTGC 637

QY 481 CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGCGCTGTACCAAGGCTTCAAGTGTCC 540
 DB 638 CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGCGCTGTACCAAGGCTTCAAGTGTCC 697
 QY 541 GTGACAGGAGATATCATCTTACACGGGGGCGCTACTTGGGGTGTACAGTACGGCCAAAGGC 600
 DB 698 GTGACAGGAGATATCATCTTACACGGGGGCGCTACTTGGGGTGTACAGTACGGCCAAAGGC 757
 QY 601 ATGCTCCCGGACCCCAAGAACACAGCATCTGTGTAGTGTGATGTATCCGACAGACCGTG 660
 DB 758 ATGCTCCCGGACCCCAAGAACACAGCATCTGTGTAGTGTGATGTATCCGACAGACCGTG 817
 QY 661 ACGGCGGTGGCGGCGT-GGTGTCTTACCCCTTTCACACAGGTGCGGCGCGCATGTATGAT 719
 DB 818 ACGGCGGTGGCGGCGTGTGGTGTCTTACACAGGTGCGGCGCGCATGTATGAT 877
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 DB 878 GCAGTCCGGGCGCAAGAGAGCTGACATCATGTACAGGGGACCGGTGATGTGGAGAA 937
 QY 780 GATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGGTGCCTGCCACGTCCTGCG 839
 DB 938 GATCTTCAGAGATGAGGGGGCAAGG-CTTCTTCAAGGGTGCCTGCTTCAAGCTCTGCG 996
 QY 840 GGGCATGGGGGCGGCT 856
 DB 997 GGGCATGGGGGCGGCTT 1013
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 LOCUS AGENCOURT 8837147 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6424804
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ933670
 VERSION BQ933670.1 GI:22349053
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 931)
 NIH-MGC http://mgc.ncl.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@p5-remail.nih.gov
 Tissue Procurement: DCTD/DFR/gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2605 row: j column: 05
 High quality sequence stop: 720.
 FEATURES
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 /db_xref="taxon:9606"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_18"
 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

BASE COUNT 173 a 307 c 287 g 164 t

Query Match 90.4%; Score 810.8; DB 13; Length 931;
 Best Local Similarity 99.0%; Pred. No. 1.3e-164;
 Matches 826; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

1 ATGACGAGACAGGACATCTCTCTCCCAAGACTTCTTGCCCGAGAGATCCCGCCGCC 60
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 97 ATGACGAGACAGGACATCTCTCTCCCAAGACTTCTTGCCCGAGAGATCCCGCCGCC 156
 |||||||
 61 ATCTCAGAGACGCGCTGCTCCGATCAGAGGGGTCAAGCTGCTGCTGAGGCTCCAGAC 120
 |||||||
 157 ATCTCAGAGACGCGCTGCTCCGATCAGAGGGGTCAAGCTGCTGCTGAGGCTCCAGAC 216
 |||||||
 121 GCCAGCAAGAGATGCTCCGCGCAAGAGATCAAGGGATCTGAGATGCTGATTCGCGC 180
 |||||||
 217 GCCAGCAAGAGATGCTCCGCGCAAGAGATCAAGGGATCTGAGATGCTGATTCGCGC 276
 |||||||
 181 ATCCCAAGAGAGAGGCGCTGCTCTCTCTGAGAGGGGCAACCTTGCCAAAGCTATTCGC 240
 |||||||
 277 ATCCCAAGAGAGAGGCGCTGCTCTCTCTGAGAGGGGCAACCTTGCCAAAGCTATTCGC 336
 |||||||
 241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGGATTAAGTCAAGAGATCTTCCG 300
 |||||||
 337 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGGATTAAGTCAAGAGATCTTCCG 396
 |||||||
 301 GGGGGGCTGGACAGACACAGAGATTTGAGAGTACTTTGGGGCAACTGGCTTCGCGC 360
 |||||||
 397 GGGGGGCTGGACAGACACAGAGATTTGAGAGTACTTTGGGGCAACTGGCTTCGCGC 456
 |||||||
 361 GGTGGGGGCGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 |||||||
 457 GGTGGGGGCGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516
 |||||||
 421 CTGGAGAGGAGAGCTGAGGAAAGTCAAGGACAGAGGCGGATTCGAGAGGCGCGGAGAGCTGCG 480
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 517 CTGGAGAGGAGAGCTGAGGAAAGTCAAGGACAGAGGCGGATTCGAGAGGCGCGGAGAGCTGCG 576
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 481 CTGGTGAAGATCAACAAAGTCCGAGGATCCGAGGCGCTGATCAAGGGCTTCAAGTGTCTCC 540
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 577 CTGGTGAAGATCAACAAAGTCCGAGGATCCGAGGCGCTGATCAAGGGCTTCAAGTGTCTCC 636
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 541 GTGCGAGGACATCATCTACCGGGGGGCTCTTCCGCGCTGATCGATCAAGGGCTTCAAGTGTCTCC 600
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 637 GTGCGAGGACATCATCTACCGGGGGGCTCTTCCGCGCTGATCGATCAAGGGCTTCAAGTGTCTCC 696
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 601 ATGCTCCCGGACCCCAAGACAGACATCGTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 660
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 697 ATGCTCCCGGACCCCAAGACAGACATCGTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 756
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 757 ACAGGCGCTGGCGCGGCTGCTCTACCCCTTCCGACAGGAGTGGGGGCGCATAGATGATG 816
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 721 CAGTCCGGGCGCAAGAGAGTCAATCATGTACAGAGGCGACCGTCACTGTTGGAGAGAG 780
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 817 CAGTCCGGGCGCAAGAGAGTCAATCATGTACAGAGGCGACCGTCACTGTTGGAGAGAG 876
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 781 ATCTTCAGAGATGAGGGGGGCAAGGCTT-CTTCAAGGCTGCTGCTCAAGCT 833
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 877 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCCAAAGGCTGCTGCTCAAGCT 930
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RESULT 15
 BX423613 1201 bp mRNA linear EST 15-MAY-2003
 LOCUS BX423613 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF034YB14.5-PRIME, mRNA sequence.
 ACCESSION BX423613
 VERSION BX423613.1 GI:30768310
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 L1 (bases 1 to 1201)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10389.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS1AF092D08P1&cluster=10389.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL : Corporation 1600
 http://fulllength.invitrogen.com/Invitrogen
 Faraday Avenue Genoscope sequence id : CS1AF092D08P1.
 Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="RNA
 /db_xref="taxon:9606"
 /clone="CS0DF034YB14"
 /issue="type="FETAL BRAIN"
 /seq_source="Fetal"
 /note="L1B-"Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT-6; 1st strand cDNA
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 29 others

BASE COUNT 236 a 364 c 357 g 215 t

Query Match 90.1%; Score 808.6; DB 13; Length 1201;
 Best Local Similarity 97.2%; Pred. No. 4.1e-164;
 Matches 872; Conservative 3; Mismatches 17; Indels 5; Gaps 5;

1 ATGACGAGACAGGACATCTCTCTCCCAAGACTTCTTGCCCGAGAGATCCCGCCGCC 60
 |||||||
 140 ATGACGAGACAGGACATCTCTCTCCCAAGACTTCTTGCCCGAGAGATCCCGCCGCC 198
 |||||||
 61 ATCTCAGAGACGCGCTGCTCCGATCAGAGGGGTCAAGCTGCTGCTGAGGCTCCAGAC 120
 |||||||
 199 ATCTCAGAGACGCGCTGCTCCGATCAGAGGGGTCAAGCTGCTGCTGAGGCTCCAGAC 258
 |||||||
 121 GCCAGCAAGAGATGCTCCGCGCAAGAGATCAAGGGATCTGAGATGCTGATTCGCGC 180
 |||||||
 259 GCCAGCAAGAGATGCTCCGCGCAAGAGATCAAGGGATCTGAGATGCTGATTCGCGC 318
 |||||||
 181 ATCCCAAGAGAGAGGCGCTGCTCTCTCTGAGAGGGGCAACCTTGCCAAAGCTATTCGC 240
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 319 ATCCCAAGAGAGAGGCGCTGCTCTCTCTGAGAGGGGCAACCTTGCCAAAGCTATTCGC 378
 |||||||
 241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGGATTAAGTCAAGAGATCTTCCG 300
 |||||||
 379 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGGATTAAGTCAAGAGATCTTCCG 438
 |||||||
 301 GGGGGGCTGGACAGACACAGAGTCTGAGAGTACTTTGGCGGCAACTTGCTCGCGC 360
 |||||||
 439 GGGGGGCTGGACAGACACAGAGTCTGAGAGTACTTTGGCGGCAACTTGCTCGCGC 498
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 361 GGTGGGGGCGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 |||||||
 499 GGTGGGGGCGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558
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 421 CTGGAGAGGAGAGTGGAGAAAGTCAAGAGAGAGGAGGAGTTCGAGGCGCTTGGAGAGATGCG 480
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 559 CTGGAGAGGAGAGTGGAGAAAGTCAAGAGAGAGGAGGAGTTCGAGGCGCTTGGAGAGATGCG 618
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QY 481 CTGTTGAAGATACCAAGTCCAGCGCATCCGGGCTTACCAGGGCTTCAGTGTCTCC 540
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Db 619 CTGGTGAAGATACCAAGTCCAGCGCATCCGGGCTTACCAGGGCTTCAGTGTCTCC 678
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QY 541 GTGCAGGGCATCATCATCTACCGGGGGGCTTCTCGGGGTGTACGATACGGCCAAAGGC 600
    |||||||
Db 679 GTGCAGGGCATCATCATCTACCGGGGGGCTTCTCGGGGTGTACGATACGGCCAAAGGC 738
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QY 601 ATGCTCCCGGACCCCAAGAACGACATCGTGTGAGCTGATGATCGCGCAGACCGTG 660
    |||||||
Db 739 ATGCTCCCGGACCCCAAGAACGACATCGTGTGAGCTGATGATCGCGCAGACCGTG 798
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QY 661 ACGGCCGTGGCCGGCGGTGTCTTACCCCTTCGACACGGTCCGGCGCCATGATGATG 720
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Db 799 ACGGCCGTGG-CCGGCGTGTGT-CTACCCCTTCGACACGGTCCGGCGCCATGATGATG 856
    |||||||
QY 721 CAGTCCGGGGCGCAAGAGAGCTGACATGATACAGGGGCAACCGTCACTGTGGAGGAG 780
    |||||||
Db 857 CAGTCCGGGGCGCAAGAGAGCTGACATGATGATACAGGGGCA-CCGTGACTGTGGAGGAG 915
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QY 781 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTCAAGGGTGCCTGCTCAACGTCTCTGCGG 840
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Db 916 AWC-TCAGAGATGAGGGGGGCAAGGCTTCTCAAGGGTGCCTGCTCAACGTCTCTGCGG 974
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QY 841 GGCATGGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
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Db 975 GCATGAGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
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Search completed: August 24, 2003, 03:33:47
 Job time : 2423 secs

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: RESULT 3
: US-09-434-354-2
: Sequence 2, Application US/09434354
: Patent No. 6562563
: GENERAL INFORMATION:
: APPLICANT: Murphy, Anne N.
: APPLICANT: Cleverger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Andreyev, Alexander Y.
: APPLICANT: Filigeri, Luciano G.
: APPLICANT: Velicelcbl, Gonul
: APPLICANT: Davis, Robert E.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
: TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
: FILE REFERENCE: 660088.433
: CURRENT APPLICATION NUMBER: US/09/434,354
: CURRENT FILING DATE: 1999-11-03
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 897
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-434-354-2

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[illegible]

Accession	Sequence	Length
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Qy	AGGGCGGTGGCGGCGGTGGTGTCTCMAACCCCTTCGACACGGTGGCGGGCCGATGATGATG	720
Dh	ACTGCTGTGTGCCGGGTGACTCTTCATTCACATTTGACACCGCTTCGCCGCGCGGATGATGATG	720
Qy	CAGTCCGGGGCGAAGGAGCTGACATCATGTATACACGGGCACTGCATCTGTGGAGGAAG	780
Dh	CAGCTCAGGGGGCGAAGGAACATACATCATGTATACACAGGCACGCTGTGACTGTGGCGGAAG	780
Qy	ATCTTAGAGATAGAGGGGGCAAGCCCTTCCTTCACAGGGTGGCTGTCCATACAGTCTCCGG	840
Dh	ATTGCTCGTGATGAAGGAGGCAAGCTTTTTCACAGGGTGGCATGCTGCATATGTTCTCAGA	840
Qy	GGCATGGGGGGCGGCTTCTGCTGTGCTCTGTACAGACAGCTTCAGGAAGGATGATCTAA	897
Dh	GGCATGGGGGGCGGCTTCTGCTGTGCTCTGTATGATGAATCAAGAAAGTACACTTA	897

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US-08-961-871-11
RESULT 4
Sequence 11, Application US/08961871
Patent No. 6013858 Issue 01-11-00
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1086
US-08-961-871-11

Query Match 65.9%; Score 591.4; DB 3; Length 1259;
Best Local Similarity 78.7%; Pred. Mismatches 122;
Matches 706; Conservative 0; Indels 0; Gaps 0;

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Mon Aug 25 09:31:43 2003

us-09-811-094-3.rni

Page 4

[illegible]

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5170 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
FEATURES:
NAME/KEY: CDS
LOCATION: 94..990
US-08-961-871-9

Query Match 65.6%; Score 588.2; DB 3; Length 1177;
Best Local Similarity 78.5%; Pred. No. 2,1e-121;
Matches 704; Conservative 0; Mismatches 193; Indels 0; Gaps 0.

1 ATGACGAAACAGGCGCATCTCTTCGCCAAGAACTTGTGGCCGGAGGAGCATGCGCGCGCC 60
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94 ATGGGGGATCATGGCTTGTGAGCTTTTATTAAGACTTCTCGSCAGGTGGCATGCGCGCGCC 153
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61 ATCTGTCAAGAGGCGCGTGTGCTCCGATTCAGGCGGGTCAAGTCTCTCTCAGTGCAGAC 120
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154 GTCCTCAAGAGCGGGGTCGCCCGCCGATGATGAGAGGGTCAAACTGCTCTCAGTGCAGAC 213
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121 GCCACACAGCAGATATCGCGCCGACACAAGAGATACAAAGGCGATGTGGAGTGCATTTGCCG 180
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214 GCCACAAAGAGATCATGTCGACAGAGAAGAGATACAAAGGCATCATTTGTTGTCGTGAGA 273
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181 ATCCCAAGAGAGCAGAGGGCGTGTCTCTTCGAGAGGGGCAACCTTGCCACATGCATATTCG 240
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274 ATCCCAAGAGAGCGGGCTTTCTCTCTTCTGAGAGGGGTAACTTGCCACATGCATATTCG 333
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241 TACTTCCCACTCAAGCCCTCAACTTGCCTTCAAGGATTAAGTACAAAGAGATCTTCTCG 300
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334 TACTTCCCACTCAAGCCCTCAAGCTTGCCTTCAAGGATTAAGTACAAAGAGATCTTCTCG 393
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301 GGGGGCGTGGACAAGACACAGCAGATTCTGAGAGTACTTTGGGGCAACTGGCCCTCGGGC 360
|||||
394 GGAGGCGTTATGCAATTAAGCAGTTCTGGGGCTACTTTGCTGTAACCTGGCCCTGTGGT 453
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361 GGTGGCGCGCGCGACGACTTCTGTGCTTGTGTAACCGCTGATTTTGGCCAGAACCGCG 420
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454 GGGGCGAGCTGGGGCCACACTCCCTCTGCTGCTGCTACCCGCTGAGACTTGTGTAAGACGAG 513
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QY 422 CTGGACGGCAGCTGGGAAAAGTCAGGCACAGAGGGCGAGTTCCGAGGCTGGGGAGATCG 480

Db 514 CTGGCTCCGCGAGCTGGCGCAAGGGATCTTCCAGCGGAGATTTCAATGGGCTGGCGAGCTGT 573

QY 481 CTGGTAGAGATCACCAAGTCGACGGCATCCGGGGGCTGTACCAAGGGCTTCAGTGTCTCC 540

Db 574 CTACCCAAAGATCTTCAAGTCGAGCGGCTGTGAAGGGTCTCTACAGGGTTCAGTGTCTT 633

QY 541 GTGCAGGGATATCATCTACCGGGGCGGCTACTTGGGCGGTACGATACGGCCAAAGGC 600

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QY 661 ACGGCGGTGGCGGGCGTGTCTCTACCCCTTCCAGACAGGTGGCGGCGCGCATGATGATG 720

Db 754 ACGGCGGTGGCGGGCGTGTGTCTTATTCGGTTTGACATGTCTCTCATAGATGATGATG 813

QY 721 CAGTCCGCGGCGCAAAAGAGACTGACATTCATGTAACAGGGCACCCTGTGCACTGTGGAGGAG 780

Db 814 CAGTCTGGCGCGCAAAAGGGCTGATTTATTTATGTAACAGGGGAGACATTGACTCTGTGAGGAG 873

QY 781 ATCTTCAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGTGCCAAGTCTGCGG 840

Db 874 ATTGCAAAAAGATGAAGAGCACCAACCTTCTTCAAGAGTGCCTGTGCCAATGTACTGAGA 933

QY 841 GGCATGGGGGGGCGCTTGTGCTGGTCCGTATGACAGCGAGCTCAAGAAGGTGATCTTA 897

Db 934 GGCATGGGTGGTCTTTTGTATTTGATTTGTAATGATGATCAAAAATATGTCTTA 990

RESULT 6
 US-09-434-354-1
 Sequence 1, Application US/09434354
 Patent No. 6562563
 GENERAL INFORMATION:
 APPLICANT: Murphy, Anne N.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Andreyev, Alexander Y.
 APPLICANT: Frigeri, Luciano G.
 APPLICANT: Velicelcbl, Gonul
 APPLICANT: Davis, Robert E.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
 TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
 TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
 FILE REFERENCE: 660088.433
 CURRENT APPLICATION NUMBER: US/09/434,354
 CURRENT FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 894
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-434-354-1

Query Match	62.9%	Pred. 564.2	DB 4	Length 894
Best Local Similarity	77.6%	Pred. No. 4e-116		
Matches 696	Conservative	0	Mismatches 198	Indels 3
				Gaps 1

[illegible][illegible]

RESULT 7
 US-09-016-434-622
 : Sequence 622, Application US/09016434
 : Patent No. 6500938
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Janice Au-Young
 : APPLICANT: Jeffrey J. Sellmer
 : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 : TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 : NUMBER OF SEQUENCES: 1490
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 : STREET: 3174 PORTER DRIVE
 : CITY: PALO ALTO
 : STATE: CALIFORNIA
 : COUNTRY: USA
 : ZIP: 94304
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: word perfect 6.1 for windows/MS-DOS 6.2

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016.434
;; FILING DATE: HEREMITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0002 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 845-4166
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 622:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 289 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: LIVERUT04
;; CLONE: 2517151
;; US-09-016-434-622

Query Match 20.7%; Score 186; DB 4; Length 289;
Best Local Similarity 99.5%; Pred. No. 1.2e-32;
Matches 197; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGAGGAAAGGAGGATCTCTTGGCCAAAGACTTCTTGGCCGAGGATCGCCGCC 60
DB 93 ATGAGGAAAGGAGGATCTCTTGGCCAAAGACTTCTTGGCCGAGGATCGCCGCC 152
QY 61 ATCTCCAGAGGCGGCTGCTCGATCGAGCGGGTCAAGTCTGCTGACAGTCCAGC 120
DB 153 ATCTCCAGAGGCGGCTGCTCGATCGAGCGGGTCAAGTCTGCTGACAGTCCAGC 212
QY 121 GCCACAGAGGATCGCGCGCGAGAGAGTCAAGAGGCGATCGATGCTATGTCGCG 180
DB 213 GCCACAGAGGATCGCGCGCGAGAGAGTCAAGAGGCGATCGATGCTATGTCGCG 271
QY 181 ATCCCAAGAGAGGCGG 198
DB 272 ATCCCAAGAGAGGCGG 289

RESULT 8
US-08-518-878B-38
; Sequence 38, Application US/08518878B
; Patent No 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: FLOPPY disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 23-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzel, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-036
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1255 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-518-878B-38

Query Match 6.3%; Score 56.4; DB 1; Length 1255;
Best Local Similarity 45.6%; Pred. No. 0.00074;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTCCGAGGCGCTGGAGACTGCTGTGAAGATCACCAAGTCCGAGGATCCGGG 515
DB 141 CGAGTCCGAGGCGCTGGAGACTGCTGTGAAGATCACCAAGTCCGAGGATCCGGG 200
QY 516 CCTGTACAGGCGCTTCAAGTCTCTCGTCAAGGCGATCATCTACCGGGGCGCTACTT 575
DB 201 CCTGTACAGGCGCTTCAAGTCTCTCGTCAAGGCGATCATCTACCGGGGCGCTACTT 260
QY 576 CGGCGGTACAGTACAGGCGGATCGTCCCGGACCCAGAGAGAGAGAGAGAGAG 635
DB 261 CGGCGGTACAGTACAGGCGGATCGTCCCGGACCCAGAGAGAGAGAGAGAGAG 320
QY 636 GAGCTGATGATCGCGCAGACCGTCAAGCGCGCGCGCGCGCGCTGCTTACCGCTTGA 695
DB 321 GAGCGGTCTCTAGCAGGCGAGCAGCAGCGTCCGCTGCTGCTGCTGCGCGCGCG 380
QY 696 CAGCGTCCGCGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 381 GAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTG 440
QY 756 GGGCAGCGCTGACTGTGTGAGAGAGATCTTCAAGATGAGAGAGAGAGAGAGAG 815
DB 441 AAGCAGCGCTGACTGTGTGAGAGAGATCTTCAAGATGAGAGAGAGAGAGAGAG 500
QY 816 GGGTGTGCTGCTCAAGCGTCTCGCGGCGATGAGAGAGAGAGAGAGAGAGAGAG 875
DB 501 AAGCAGCGCTGCTCAAGCGTCTCGCGGCGATGAGAGAGAGAGAGAGAGAGAGAG 560
QY 876 CGAGCTCAGAGAG 889
DB 561 TGACCTCATCAGAG 574

RESULT 9
US-08-294-522B-38
; Sequence 38, Application US/08294522B
; Patent No 5741666
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: FLOPPY disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-522B-38

Query Match      6.3%; Score 56.4; DB 1; Length 1255;
Best Local Similarity 45.6%; Pred. No. 0.00074;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTCCGAGCGCTGGAGACGCTGTTGAAGATCACCAAGTCCGAGGGCATCGGGG 515
DB 141 CCAGTACCCGCGGTGATGAGGCACTTCTGACCATGTGCGTACTGAGGGCCCCGGAAG 200
QY 516 CCGTACCAAGGCTTCAGTCTCCGTGCGAGGCGCATCATCTACCGGGCGGCTACTT 575
DB 201 CCTCTCAATAGGGCTGTTGCCGGCTCGAGCGCCAAATAGAGCTTGCTGTGTCCGAT 260
QY 576 CGGCGTACGATACGCGCAAGGCGATGCTCCCGGACCCCAAGACAGCAGCATGCTGT 635
DB 261 CGGCGTATGATTTGTCAAAACAGTTTCACCAAGGGCTCTGACATGCGCAGCATTTG 320
QY 636 GAGCTGATGATGCGCAGACCGTGCAGCGGCGGCGGCGGTGCTCTCAACCTTCGA 695
DB 321 GAGCGCCCTCTTACGACGAGCAGCACAGTGCCTGCTGTGCTGTGCGCCAGCCAC 380
QY 696 CAGCGTGGCGGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 381 GATGTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 440
QY 756 GGGCAGCGTGCAGTGTGAGAGAAATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAA 815
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QY 816 GGGTGGTGGTCAAGCTCTGCGGGGCGCATGGGGGCGCTTCGTCGTGCTGTACGA 875
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RESULT 10
US-08-470-868A-38
; Sequence 38, Application US/08470868A
; Patent No. 5861485
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis C.
; TITLE OF INVENTION: Compositions and Methods for the
; TITL OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-38

Query Match      6.3%; Score 56.4; DB 2; Length 1255;
Best Local Similarity 45.6%; Pred. No. 0.00074;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTCCGAGCGCTGGAGACGCTGTTGAAGATCACCAAGTCCGAGGGCATCGGGG 515
DB 141 CCAGTACCCGCGGTGATGAGGCACTTCTGACCATGTGCGTACTGAGGGCCCCGGAAG 200
QY 516 CCGTACCAAGGCTTCAGTCTCCGTGCGAGGCGCATCATCTACCGGGCGGCTACTT 575
DB 201 CCTCTCAATAGGGCTGTTGCCGGCTCGAGCGCCAAATAGAGCTTGCTGTGTCCGAT 260
QY 576 CGGCGTACGATACGCGCAAGGCGATGCTCCCGGACCCCAAGACAGCAGCATGCTGT 635
DB 261 CGGCGTATGATTTGTCAAAACAGTTTCACCAAGGGCTCTGACATGCGCAGCATTTG 320
QY 636 GAGCTGATGATGCGCAGACCGTGCAGCGGCGGCGGCGGTGCTCTCAACCTTCGA 695
DB 321 GAGCGCCCTCTTACGACGAGCAGCACAGTGCCTGCTGTGCTGTGCGCCAGCCAC 380
QY 696 CAGCGTGGCGGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 381 GATGTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 440
QY 756 GGGCAGCGTGCAGTGTGAGAGAAATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAA 815
DB 441 AAGCAGCGTCAATGCTTACAAAGACATTCGCCGAGGAAAGGTTCCGGGGCTCTGGA 500
QY 816 GGGTGGTGGTCAAGCTCTGCGGGGCGCATGGGGGCGCTTCGTCGTGCTGTACGA 875
DB 501 AGGAGCTCTCCCAATGTTGCTGTATGATGATGATGATGATGATGATGATGATG 560
QY 876 CGAGCTCAAGAAAG 889
DB 561 TGACCTCATCAAGG 574

RESULT 11
US-08-807-861A-38
; Sequence 38, Application US/08807861A
; Patent No. 5853975
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITL OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-807-861A-38

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Query Match
Best Local Similarity 45.6%; Score 56.4; DB 2; Length 1596;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;
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483 CCAGTACCGGGGTGTGTGGGACCACTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTG 542
516 CCGTACCGAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575
543 CCGTACCAATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
576 CGGCGGTACAGTACGCGCCAGGAGGATGCTCCCGACCCCAAGAACACGACATGCTGT 635
603 CGGCTGTATGATTTCTGTCAAAAGTCTTACACCAAGGCTTGAACATGACATGACATG 662
636 GAGCTGATATGCGCAGACGATGAGCGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 695
663 GAGCGGCTCTTGAAGGAGGACCAAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
696 CAGGCTGGGGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
723 GAGTGTGTAAAGTCCGATTCGACAGCTCAGCCCGGCTGAGAGTGTGAGAGTATACCA 782
756 GGGACGCTGACTGTGAGAGAAATCTTCAAGATGAGGGGGGCAAGGCTTCTTCAA 815
783 AAGCACCCTCAATGCTTACCAAGACCATGCGGAGAGAGAGGCTTCCGGGGCTCTGGA 842
816 GGGTGGCTGCTCAACGCTCCCTGGGGGATGAGGGGGGCGCTTGTGCTGCTGCTGCTGCA 875
843 AGGACCTCTCCCAATGTTGCTGTAAATGATGATGATGATGATGATGATGATGATGATGAT 902
876 CGAGCTCAAGAGG 889
903 TGACCTCATCAAG 916

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RESULT 12
US-09-210-681-38
Sequence 38, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
Applicant: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Pennine & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-210-681-38

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Query Match
Best Local Similarity 45.6%; Score 56.4; DB 3; Length 1596;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;
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483 CCAGTACCGGGGTGTGTGGGACCACTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTG 542
516 CCGTACCGAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575
543 CCGTACCAATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
576 CGGCGGTACAGTACGCGCCAGGAGGATGCTCCCGACCCCAAGAACACGACATGCTGT 635
603 CGGCTGTATGATTTCTGTCAAAAGTCTTACACCAAGGCTTGAACATGACATGACATG 662
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663 GAGCGGCTCTTGAAGGAGGACCAAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
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Db 723 GGATGTGGTAAGTCCATTCACAGTCACGGCCGGGCTGAGAGTGTGGAGATACCA 782
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Db 783 AAGCACCTCTCCCAATGCTTACAGAACCATTCGCCGAGAGAGAGGTTCCGGGGCCCTCTGGAA 842
Qy 816 GGGTGGTGTGTCACAGTCTCTGCGGGGATGAGGGGCGCCCTTCGTGCTGTCTGTAGACA 875
Db 843 AGGAGACCTCTCCCAATGCTTCTGTATGTCATTCATCTGTGCTGAGCTGTGTACCTTA 902
Qy 876 CGAGCTCAAGAG 889
Db 903 TGACCTCATCAAG 916

RESULT 13
US-08-946-719A-38
Sequence 38, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-946-719A-38

Query Match 5.3%; Score 56.4; DB 3; Length 1596;
Best Local Similarity 45.6%; Pred. No. 0.00078;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

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Db 483 CCAGTACCGCGGTGTGATGGGACCATTTGTGACCATGTGTGCTGAGGGCCCGCGAAG 542

Qy 516 CCTGTACAGGCGCTTCACTGTCTCCGTGACGGGATCATCATACCGGGCGGCTACTT 575
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Qy 576 GGGCGTGTACATAGCGCCCAAGGAGATGCTCCCGACCCCAAGAAACAGCAATGTGT 635
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Db 723 GGATGTGGTAAGTCCATTCACAGTCACGGCCGGGCTGAGAGTGTGGAGATACCA 782
Qy 756 GGGCACCCCTGCAGCTTTGGAGAGATCTTCAGAGATGAGGGGCGCAAGCCCTTCTTCAA 815
Db 783 AAGCACCTCTCCCAATGCTTACAGAACCATTCGCCGAGAGAGGTTCCGGGGCCCTCTGGAA 842
Qy 816 GGGTGGTGTGTCACAGTCTCTGCGGGGATGAGGGGCGCCCTTCGTGCTGTCTGTAGACA 875
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Db 903 TGACCTCATCAAG 916

RESULT 14
US-09-547-983-38
Sequence 38, Application US/09547983
Patent No. 6518402
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,983
FILING DATE: 12-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 03:33:53 ; Search time 252 Seconds
(without alignments)
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Title: US-09-811-094-3

Perfect score: 897
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	897	100.0	897	10	US-09-185-904A-3
4	895.4	99.8	1212	14	US-10-037-270-687
5	873.4	97.4	2592	13	US-10-044-090-152
6	771.2	86.0	1116	10	US-09-969-708-213
7	771.2	86.0	1116	14	US-09-880-107-2096
8	771.2	86.0	1116	14	US-10-171-581-48
9	596.2	66.5	1196	10	US-09-917-800A-1327
10	594.6	66.3	897	9	US-09-811-094-2
11	594.6	66.3	897	9	US-09-810-644-2
12	594.6	66.3	897	10	US-09-185-904A-2
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	23	334	37.2	420	11	US-09-918-995-5524	Sequence 5524, App
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ALIGNMENTS

RESULT 1
US-09-811-094-3
Sequence 3, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleverger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
US-09-811-094-3

Query Match 100.0%; Score 897; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 5.3e-227;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 601 ATGCTCCCGCAGCCCAAGAACACGACATCTGTGTAGCTGTAGTATGCGCAGACGCTG 660
OY 661 ACGGCCCTGTGCGCGCGCTGTGTCTTACCCCTTTCAGACAGGTCGCGCGCGCGCGCG 720
    |||
    |||
    |||
Db 661 ACGGCCCTGTGCGCGCGCTGTGTCTTACCCCTTTCAGACAGGTCGCGCGCGCGCGCG 720
OY 721 CAGTCCCGCGCGCAAGAGCAGTACATCTTCAAGGCTGCGTGTACAGCAGTCTTCAAG 780
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    |||
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Db 721 CAGTCCCGCGCGCAAGAGCAGTACATCTTCAAGGCTGCGTGTACAGCAGTCTTCAAG 780
OY 781 ATCTTCAAGATGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
    |||
    |||
    |||
Db 781 ATCTTCAAGATGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
OY 841 GGCATGGGGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 897
    |||
    |||
    |||
Db 841 GGCATGGGGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 897

RESULT 2
US-09-810-644-3
; Sequence 3, Application US/09810644
; Patent No. US2002001292A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davls, Robert E.
; APPLICANT: Cleveland, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; FILE REFERENCE: 660088.42003
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-644-3
Query Match      100.0%; Score 897; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 5.3e-227;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTCTTGGCGGAGGCGCATGCGCGCGCG 60
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    |||
    |||
Db 1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTCTTGGCGGAGGCGCATGCGCGCGCG 60
OY 61 ATCTCAAGAGCGCGCGTCCGATCGAGCGGTCAAGCTGTCTGTGAGTCTGAGTCTGAGCAG 120
    |||
    |||
    |||
Db 61 ATCTCAAGAGCGCGCGTCCGATCGAGCGGTCAAGCTGTCTGTGAGTCTGAGTCTGAGCAG 120
OY 121 GCCAGCAGCAGATGCGCGCGCGCAGCAGTACAGAGGCGATCTGAGTCTGAGTCTGAGCAG 180
    |||
    |||
    |||
Db 121 GCCAGCAGCAGATGCGCGCGCGCAGCAGTACAGAGGCGATCTGAGTCTGAGTCTGAGCAG 180
OY 181 ATCCCAAGAGCAGAGGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
    |||
    |||
    |||
Db 181 ATCCCAAGAGCAGAGGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
OY 241 TACTTCCCACTCAAGCCCTCACTGCGCTTCAGAGATTAAGTACAGCAGATCTTCCTG 300
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    |||
    |||
Db 241 TACTTCCCACTCAAGCCCTCACTGCGCTTCAGAGATTAAGTACAGCAGATCTTCCTG 300
OY 301 GGGGGGCGTGAGACAGCAGCAGTCTGAGAGTCTTGAGGCGCACTGGGCACTGGCGCG 360
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    |||
    |||
Db 301 GGGGGGCGTGAGACAGCAGCAGTCTGAGAGTCTTGAGGCGCACTGGGCACTGGCGCG 360
OY 361 GGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
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    |||
Db 361 GGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
OY 421 CTGCGCAGCGAGCTGAGGAGAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
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    |||
    |||
Db 421 CTGCGCAGCGAGCTGAGGAGAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
OY 481 CTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
    |||
    |||
    |||
Db 481 CTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
OY 541 GTGCGAGGCGATCATCTTACCGGCGCGCTTACTTCCGCGTGTACAGATTAAGGCGCG 600
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    |||
    |||
Db 541 GTGCGAGGCGATCATCTTACCGGCGCGCTTACTTCCGCGTGTACAGATTAAGGCGCG 600
OY 601 ATGCTCCCGCAGCCCAAGAACACGACATCTGTGTAGCTGTAGTATGCGCAGACGCTG 660
    |||
    |||
    |||
Db 601 ATGCTCCCGCAGCCCAAGAACACGACATCTGTGTAGCTGTAGTATGCGCAGACGCTG 660
OY 661 ACGGCCCTGTGCGCGCGCTGTGTCTTACCCCTTTCAGACAGGTCGCGCGCGCGCGCG 720
    |||
    |||
    |||
Db 661 ACGGCCCTGTGCGCGCGCTGTGTCTTACCCCTTTCAGACAGGTCGCGCGCGCGCGCG 720
OY 721 CAGTCCCGCGCGCAAGAGCAGTACATCTTCAAGGCTGCGTGTACAGCAGTCTTCAAG 780
    |||
    |||
    |||
Db 721 CAGTCCCGCGCGCAAGAGCAGTACATCTTCAAGGCTGCGTGTACAGCAGTCTTCAAG 780
OY 781 ATCTTCAAGATGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
    |||
    |||
    |||
Db 781 ATCTTCAAGATGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
OY 841 GGCATGGGGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 897
    |||
    |||
    |||
Db 841 GGCATGGGGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 897

RESULT 3
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US-09-185-904A-3
 ; Sequence 3, Application US/09185904A
 ; Patent No. US2002017185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Cleverger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185,904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 897
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-185-904A-3

Query Match 100.0%; Score 897; DB 10; Length 897;
 Best Local Similarity 100.0%; Pred. No. 5.3e-227;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGGGAACAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 60
 1 ATGAGGGAACAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 60
 61 ATCTCAAGACGCGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 120
 61 ATCTCAAGACGCGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 120
 61 ATCTCAAGACGCGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 120
 121 GCCAGCAAGCAGATGCGCGCGCAAGAGTACAAAGGCGATCTGATGTCGCGC 180
 121 GCCAGCAAGCAGATGCGCGCGCAAGAGTACAAAGGCGATCTGATGTCGCGC 180
 121 GCCAGCAAGCAGATGCGCGCGCAAGAGTACAAAGGCGATCTGATGTCGCGC 180
 181 ATCCCAAGGAGCAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 240
 181 ATCCCAAGGAGCAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 240
 241 TACTTCCCAAGCAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 300
 241 TACTTCCCAAGCAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 300
 301 GGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 360
 301 GGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 360
 301 GGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 360
 361 GGTGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 420
 361 GGTGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 420
 421 CTGGAGCGGAGCAGTGGGAGTCAAGAGCAGAGCAGTCTTGGCGGAGCATCCCGCGGC 480
 421 CTGGAGCGGAGCAGTGGGAGTCAAGAGCAGAGCAGTCTTGGCGGAGCATCCCGCGGC 480
 481 CTGGAGCGGAGCAGTGGGAGTCAAGAGCAGAGCAGTCTTGGCGGAGCATCCCGCGGC 540
 481 CTGGAGCGGAGCAGTGGGAGTCAAGAGCAGAGCAGTCTTGGCGGAGCATCCCGCGGC 540
 541 GGTGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 600
 541 GGTGGGCGGTGAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 600
 601 ATGCTCCCGGAGCAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 660
 601 ATGCTCCCGGAGCAGCAGCAGCAGTCTGAGGATCTTGGCGGAGCATCCCGCGGC 660

661 ACGCCGTGGCGCGCGCTGCTCTACCCCTTGCAGACGCTGCGCGCGCATGATGATG 720
 661 ACGCCGTGGCGCGCGCTGCTCTACCCCTTGCAGACGCTGCGCGCGCATGATGATG 720
 721 CAGTCCGGGCGCAAGGAGCTGACATGATGACGAGGAGCGCTGCTGAGGAGGAG 780
 721 CAGTCCGGGCGCAAGGAGCTGACATGATGACGAGGAGCGCTGCTGAGGAGGAG 780
 781 ATCTTCAGAGATGAGGAGGAGCAGGCTCTTCAAGAGGATGCTGCTCAAGCTCTGCGG 840
 781 ATCTTCAGAGATGAGGAGGAGCAGGCTCTTCAAGAGGATGCTGCTCAAGCTCTGCGG 840
 841 GGCATGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 841 GGCATGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

RESULT 4

US-10-037-270-687
 ; Sequence 687, Application US/10037270
 ; Publication No. US20030104529A1
 ; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aldong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Pian
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dairui
 APPLICANT: Wang, Zhilwei
 APPLICANT: Tillinghast, John
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/10/037,270
 CURRENT FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1104
 SOFTWARE: PL_genes Version 1.0
 SEQ ID NO 687
 LENGTH: 1212
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (131)..(1027)
 US-10-037-270-687

Query Match 99.8%; Score 895.4; DB 14; Length 1212;
 Best Local Similarity 99.8%; Pred. No. 1.4e-226;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGAGGGAACAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 60
 131 ATGAGGGAACAGGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 190
 61 ATCTCAAGACGCGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 120
 191 ATCTCAAGACGCGCGCTCTCTCCCAAGACTTCTTGGCGGAGCATCCCGCGGC 250
 121 GCCAGCAAGCAGATGCGCGCGCAAGAGTACAAAGGCGATCTGATGTCGCGC 180

Db	251	GGCAGCAGAGATCGCCGCCGCACAGAGATCAAGAGGACATCGGAGACTGCTATTCGCG	310
Oy	181	ATCCCCAAGGAGCAGGGGCGTGTGTCTCTTGTGGAGGGGCAACCTTGCACAGCATTTGGC	240
Db	311	ATCCCAAGAGAGCAGGGCGTGTGTCTCTTGTGGAGGGGCAACCTTGCACAGCATTTGGC	370
Oy	241	TACTTCCCACTCAAGGCCCTCAACTTGGCTGTCAAGGATTAATGATCAAGAGATTTCTCG	300
Db	371	TACTTCCCACTCAAGGCCCTCAACTTGGCTGTCAAGGATTAATGATCAAGAGATTTCTCG	430
Oy	301	GGGGCGCTGTGACAGACACACGACAGTTCTTGGAGATTACTTTGGGGCAACTCGGCTCCGGC	360
Db	431	GGGGCGCTGTGACAGACACACGACAGTTCTTGGAGATTACTTTGGGGCAACTCGGCTCCGGC	490
Oy	361	GGTGGGGCGGGCGGACCTCCCTGTGCTTTCGTGTACCCGCTGTGATTTTGGCAAGACCGCG	420
Db	491	GGTGGGGCGGGCGGACCTCCCTGTGCTTTCGTGTACCCGCTGTGATTTTGGCAAGACCGCG	550
Oy	421	CTGGCAGCGGACGTGTGGGAAAGTACGACACAGACGCGAGTTCGAGGCGCTGGAGACTGC	480
Db	551	CTGGCAGCGGACGTGTGGGAAAGTACGACACAGACGCGAGTTCGAGGCGCTGGAGACTGC	610
Oy	481	CTGTGTGAAGATCAACCAAGTCCGACGGGACATCCGGGGCGCTGTACAGGGCTTCACTGTCTCC	540
Db	611	CTGTGTGAAGATCAACCAAGTCCGACGGGACATCCGGGGCGCTGTACAGGGCTTCACTGTCTCC	670
Oy	541	GTGCAAGGACATCACTACCGGGGGGCGTCTACTTCCGCGGTGTACGATACGAGGCAAGGGC	600
Db	671	GTGCAAGGACATCACTACCGGGGGGCGTCTACTTCCGCGGTGTACGATACGAGGCAAGGGC	730
Oy	601	ATGCTCTCCCGACCCCAAGAACACAGACGACATCTGTGTGAGTCTGATGAATCGGACGACCTGTG	660
Db	731	ATGCTCTCCCGACCCCAAGAACACAGACGACATCTGTGTGAGTCTGATGAATCGGACGACCTGTG	790
Oy	661	ACGGGCGGTGTGGCGGCGGTGTGTCTCTACCCCTTCGACACAGGTGTGGGGCGGCATGATGATG	720
Db	791	ACGGGCGGTGTGGCGGCGGTGTGTCTCTACCCCTTCGACACAGGTGTGGGGCGGCATGATGATG	850
Oy	721	CAGTCCGGGGCCCAAGAGAGCTGACATCAATGATACAGGGGACCGTGTGAGTCTTGGAGAGAG	780
Db	851	CAGTCCGGGGCCCAAGAGAGCTGACATCAATGATACAGGGGACCGTGTGAGTCTTGGAGAGAG	910
Oy	781	ATCTTCAGATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGCTGTGTCAACGCTCTCGCG	840
Db	911	ATCTTCAGATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGCTGTGTCAACGCTCTCGCG	970
Oy	841	GGCATGGGGGGCGGCTTGT	897
Db	971	GGCATGGGGGGCGGCTTGT	1027
RESULT 5			
US-10-044-090-152			
Sequence 152, Application US/10044090			
Publication No. US20020137081A1			
GENERAL INFORMATION:			
APPLICANT: Olga Bandman			
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION			
FILE REFERENCE: PA-0028 US			
CURRENT APPLICATION NUMBER: US/10/044, 090			
CURRENT FILING DATE: 2002-01-09			
NUMBER OF SEQ ID NOS: 850			
SOFTWARE: PERL Program			
SEQ ID NO 152			
LENGTH: 2592			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURES:			
NAME/KEY: misc_feature			
OTHER INFORMATION: Inbyte ID No. US20020137081A1 1330214.11			
NAME/KEY: unsure			
LOCATION: 1131, 1929			
OTHER INFORMATION: a, t, c, g, or other			

Query Match	97.4%	Score 873.4	DB 13	Length 2592
Best Local Similarity	99.7%	Pred. No. 9,9e-221		
Matches	896	Conservative	0	Mismatches 1; Indels 2; Gaps 2;
QY	1	ATGACGGAAACAGCCCATCTCCCTGCGCCCAAGAACTCTTGTGGCCGAGGAGAT-CGCCCCC	59	
Db	207	ATGACGGAAACAGCCCATCTCTCTTGGCCCAAGAACTCTTGTGGCCGAGGAGATCGCCCCC	266	
QY	60	CATCTCCAAACGGCCCGTGGCTGCGCATTCAGC-GGGTCAAGCTGCTGTCAAGTTCAC	118	
Db	267	CATCTCCAAACGGCCCGTGGCTGCGCATTCAGC-GGGTCAAGCTGCTGTCAAGTTCAC	326	
QY	119	ACGCCACAAAGCAGATTCGCGCCGCCCAACAGCAATGACAAAGGGCATCGTAGCGCATTTGTC	178	
Db	327	ACGCCACAAAGCAGATTCGCGCGCCGCCCAACAGCGATGACAAAGGGCATCGTAGCGCATTTGTC	386	
QY	179	GCATCTCCCAAGAGACAGGGCGTGTCTTCTTGTGAGGGGCAACTTGTCCAAAGTATTC	238	
Db	387	GCATCTCCCAAGAGAGAGGGCGTGTCTTCTTGTGAGGGGCAACTTGTCCAAAGTATTC	446	
QY	239	GCTACTTCTCCCATCAAGCCCTCAACTTGGCTTCAAGGATTAATGACAGCATCTTCC	298	
Db	447	GCTACTTCTCCCATCAAGCCCTCAACTTGGCTTCAAGGATTAATGACAGCATCTTCC	506	
QY	299	TGGGGGGCGTGGCAAGCAGCAGCATTTCTGAGAGTACTTTGCGGCAACTGTGCTCCG	358	
Db	507	TGGGGGGCGTGGCAAGCAGCAGCATTTCTGAGAGTACTTTGCGGCAACTGTGCTCCG	566	
QY	359	GGGCTGCGGCGCGGCGGACCTCCCTCTCTCTTCTGTATACCGCGTGAATTTTCCAGAACCC	418	
Db	567	GGGCTGCGGCGCGGCGGACCTCCCTCTCTCTCTGTGTATACCGCGTGAATTTTCCAGAACCC	626	
QY	419	GCCTGGCAGCGGAGCAGTGGGAAAGTATAGCAGACAGAGCGCAGTTCGAGGCGCTGGAGACT	478	
Db	627	GCCTGGCAGCGGAGCAGTGGGAAAGTATAGCAGACAGAGCGCAGTTCGAGGCGCTGGAGACT	686	
QY	479	GCCTGGTGAAGATATACCAAGTCCGACGGGCATCCGGGGCGCTGTACCAAGGGCTTCAGTGTCT	538	
Db	687	GCCTGGTGAAGATATACCAAGTCCGACGGGCATCCGGGGCGCTGTACCAAGGGCTTCAGTGTCT	746	
QY	539	CGGTGACAGGGGATCATCATCTACGGGGGGGCGCTACTTTCGGCGGTATACATACGGGCCAAAG	598	
Db	747	CGGTGACAGGGGATCATCATCTACGGGGGGGCGCTACTTTCGGCGGTATACATACGGGCCAAAG	806	
QY	599	GCATCTCTCCCGAACCCCAAGAACACGCGCATCTGTGTGAGTGTGATGTGCGCGACACCG	658	
Db	807	GCATCTCTCCCGAACCCCAAGAACACGCGCATCTGTGTGAGTGTGATGTGCGCGACACCG	866	
QY	659	TGACGGCGGTGGCGGGCGTGTGTCTTACCGCTTTCGACACAGGTGGGGGGCGCGATATATGA	718	
Db	867	TGACGGCGGTGGCGGGCGTGTGTCTTACCGCTTTCGACACAGGTGGGGGGCGCGATATATGA	926	
QY	719	TTCAGTCCGGGCGCAAGAGAGTGCATCATATGTACACGGGCGACCTGCATCTGTGGAGGA	778	
Db	927	TTCAGTCTCCGGGCGCAAGAGAGTGCATCATATGTACACGGGCGACCTGCATCTGTGGAGGA	986	
QY	779	AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGAGGTGTGTGTCCAAAGTCTCTGC	838	
Db	987	AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGAGGTGTGTGTCCAAAGTCTCTGC	1044	
QY	839	GGGGGATGGGGGGCGCTTCTGTGTGTCTGTACGACGAGCTCAAGAGGATGTATCTAA	897	
Db	1047	GGGGGATGGGGGGCGCTTCTGTGTGTCTGTACGACGAGCTCAAGAGGATGTATCTAA	1105	

Qy	ATCGCGGAGACCGTGAACGGCCGTGGCCGGCTGTGTTCTCAACCCCTTCACACGGTGGG	703
Db	ATCGCGGAGACCGTGAACGGCCGTGGCCGGCTGTGTTCTCAACCCCTTCACACGGTGGG	597
Qy	644 ATCGCGGAGACCGTGAACGGCCGTGGCCGGCTGTGTTCTCAACCCCTTCACACGGTGGG	
Db	538 ATCGCGGAGACCGTGAACGGCCGTGGCCGGCTGTGTTCTCAACCCCTTCACACGGTGGG	
Qy	706 CGGGCCATGATGATGACGATCGCGGGGCGAAAGAGACTGACATCATGACAGGGGACGCTC	765
Db	598 CGGGCCATGATGATGACGATCGCGGGGCGAAAGAGACTGACATCATGACAGGGGACGCTC	657
Qy	766 GACCTCTGGAGAGAAATCTTTCAGAAATGAGGGGGCGAAAGGCTCTTTCAAAGGTCGCTGG	825
Db	658 GACCTCTGGAGAGAAATCTTTCAGAAATGAGGGGGCGAAAGGCTCTTTCAAAGGTCGCTGG	717
Qy	826 TCCAACTGCTCTGCGGGGCATGGGGGCGCTTCTGTGTCCTGTAGACGAGCTCAAG	885
Db	718 TCCAACTGCTCTGCGGGGCATGGGGGCGCTTCTGTGTCCTGTAGACGAGCTCAAG	777
Qy	886 AAGTGATCTTAA 897	
Db	778 AAGTGATCTTAA 789	

RESULT 8
US-10-171-581-48
Sequence 48, Application US/10171581
Publication NO. US20030104426A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Linley, Peter
APPLICANT: Mao Mao
TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
FILE REFERENCE: 9301-117-899
CURRENT APPLICATION NUMBER: US/10/171,581
CURRENT FILING DATE: 2002-06-14
PRIORITY FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 366
SEQ ID NO 48
LENGTH: 1116
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: J03592
DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-48

Query Match	Similarity	86.0%	Score	771.2	DB	14	Length	1116
Best Local	Similarity	99.2%	Pred. No.	7.9e-194				
Matches	786	Conservative	0	Mismatches	3	Indels	3	Gaps
Qy	106	CTGCAGGTCGACAGACCGACGACGAGAGTCGCCGCCGACAGCACTACAAAGGATCTG	165					
Db	1	CTGCAGGTCGACAGACCGACGACGAGAGTCGCCGCCGACAGCACTACAAAGGATCTG	60					
Qy	166	GACATGCAATTCCTCCGATCCCGAAGAGAGCGGCTCTGCTCTTGTGAGAGGGCACTT	225					
Db	61	GACATGCAATTCCTCCGATCCCGAAGAGAGCGGCTCTGCTCTTGTGAGAGGGCACTT	120					
Qy	226	GCCAACTGCTAATTCGCTACTTCCCACTCAAGCCCTCAACTTGGCTTCAGATTAAGTAC	285					
Db	121	GCCAACTGCTAATTCGCTACTTCCCACTCAAGCCCTCAACTTGGCTTCAGATTAAGTAC	180					
Qy	286	AAGCAGATCTTCTCGGGGGGCGTGACACACACGACGACTGTGGAGGTACTTTCGGGC	345					
Db	181	AAGCAGATCTTCTCGGGGGGCGTGACACACGACGACTGTGGAGGTACTTTCGGGC	237					
Qy	346	AACCTGGACCTCGAGCGGTGCGGCGCGGCGACCTCCCTCTGTTTGTGTACCCGCTGGAT	405					
Db	238	AACCTGGACCTCGAGCGGTGCGGCGCGGCGACCTCCCTCTGTTTGTGTACCCGCTGGAT	297					
Qy	406	TTTTCACGAACCCGCGCTGGCAGCGGACCTGGAGAAATCTAGGACACGAGACGGGAGTTCCCA	465					
Db	298	TTTTCACGAACCCGCGCTGGCAGCGGACCTGGAGAAATCTAGGACACGAGACGGGAGTTCCCA	357					

OY	466	GGCCCTGGGAGATCTCCCTGGTGAAGATCAACAAGTCGAGAGGATCCGGGGCCTGTACAG	525b
Db	358	GGCCCTGGGAGATCTCCCTGGTGAAGATCAACAAGTCGAGAGGATCCGGGGCCTGTACAG	417b
OY	526	GGCTCAGTGTCTCCGTCGAGGGGACATCATCTACAGGGGGGCTACTTGGGGGTAC	585b
Db	418	GGCTCAGTGTCTCCGTCGAGGGGACATCATCTACAGGGGGGCTACTTGGGGGTAC	477b
OY	586	GATPAGGCGAAGGGCATGCTCCGCCGACCCCAAGAAACAACGACATCGTGTAGCTGTATG	645b
Db	478	GATPAGGCGAAGGGCATGCTCCGCCGACCCCAAGAAACAACGACATCGTGTAGCTGTATG	537b
OY	646	ATCCGGGAGACCGTGAAGGCGCTGGCGGGGTGTCTCACTCCCTTGACACAGGTGCGG	705b
Db	538	ATCCGGGAGACCGTGAAGGCGCTGGCGGGGTGTCTCACTCCCTTGACACAGGTGCGG	597b
OY	706	CGGGCGATGATGATGCAGTCCGGGGCGCAAGAGACTATCATCTGTACACGGGCAAGCTC	765b
Db	598	CGGGCGATGATGATGCGAGTCCGGGGCGCAAGAGACTATCATCTGTACACGGGCAAGCTC	657b
OY	766	GACTCTTGGAGGAAGATCTTCACAGAGTGAAGGGGGCAAGGCCCTTCTTCAGAGGGTGCCTG	825b
Db	658	GACTCTTGGAGGAAGATCTTCACAGATGAAGGGGGCAAGGCCCTTCTTCAGAGGGTGCCTG	717b
OY	826	TCCCAACGTCTCGCGGGGACATGGGGGGCCCTTCGTGCTGTCTGTACAGCAGAGCTCAAG	885b
Db	718	TCCCAACGTCTCGCGGGGACATGGGGGGCCCTTCGTGCTGTCTGTACAGCAGAGCTCAAG	777b
OY	886	AAGGTGATCTAA 897	
Db	778	AAGGTGATCTAA 789	

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1  RESULT 917-800A-1327
2  US-09-917-800A-1327
3  : Sequence 1327, Application US/09917800A
4  : Patient No. US20020119462A1
5  : GENERAL INFORMATION:
6  : APPLICANT: Mendrick, Donna
7  : APPLICANT: Porter, Mark
8  : APPLICANT: Johnson, Kory
9  : APPLICANT: Castle, Arthur
10 : APPLICANT: Elshoff, Michael
11 : APPLICANT: Gene Logic Inc.
12 : TITLE OF INVENTION: Molecular Toxicology Modeling
13 : FILE REFERENCE: 44921-5038-US
14 : CURRENT APPLICATION NUMBER: US/09/917,800A
15 : PRIOR FILING DATE: 2001-07-31
16 : PRIOR APPLICATION NUMBER: US 60/222,040
17 : PRIOR FILING DATE: 2000-07-31
18 : PRIOR APPLICATION NUMBER: US 60/222,880
19 : PRIOR FILING DATE: 2000-11-02
20 : PRIOR APPLICATION NUMBER: US 60/290,029
21 : PRIOR FILING DATE: 2001-05-11
22 : PRIOR APPLICATION NUMBER: US 60/290,645
23 : PRIOR FILING DATE: 2001-05-15
24 : PRIOR APPLICATION NUMBER: US 60/292,336
25 : PRIOR FILING DATE: 2001-05-22
26 : PRIOR APPLICATION NUMBER: US 60/295,798
27 : PRIOR FILING DATE: 2001-06-06
28 : PRIOR APPLICATION NUMBER: US 60/297,457
29 : PRIOR FILING DATE: 2001-06-13
30 : PRIOR APPLICATION NUMBER: US 60/298,884
31 : PRIOR FILING DATE: 2001-06-19
32 : PRIOR APPLICATION NUMBER: US 60/303,459
33 : PRIOR FILING DATE: 2001-07-09
34 : NUMBER OF SEQ ID NOS: 1740
35 : SOFTWARE: PatentIn Ver. 2.1
36 : SEQ ID NO 1327
37 : LENGTH: 1196
38 : TYPE: DNA
39 : ORGANISM: Rattus norvegicus

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FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D12770
; US-09-917-800A-1327

Query Match      66.5%; Score 596.2; DB 10; Length 1196;
Best Local Similarity 79.0%; Pred. No. 1.1e-147;
Matches 709; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 1 ATGACGGAACAGCCATCTCTTCCGCAAAAGACTTCTTGCCGAGGAGCATCCGCGCC 60
DB ATGGGGGATCAGAGCTTTAGCTTCTCTTAGAGACTTCTTGAGAGTCCGCGCGCC 135
QY 61 ATCTCCAGAGCGCGCTGCTCCGATCGAGCGGTCAGCTCTGCTGAGTCCAGCAC 120
DB ATCTCCAGAGCGCGCTGCTCCGATCGAGCGGTCAGCTCTGCTGAGTCCAGCAC 195
QY 121 GCCAGCAGCAGATGCGCGCGACAAAGCTCAAGGGGATGCTGAGCATTTGCGGC 180
DB GCCAGCAGCAGATGCGCGCGACAAAGCTCAAGGGGATGCTGAGCATTTGCGGC 255
QY 181 ATCCCAAGAGAGAGCGGCTGCTCTCTTCTGAGGGGCAACCTTGCAACGTCATTCGC 240
DB ATCCCAAGAGAGAGCGGCTTCTCTCTCTGAGGGGTAACCTTGCAACGTCATTCGC 315
QY 241 TACTTCCGACACCAAGCCCTCAACTTCGCTTCAAGAGATTAAGTACAGCATCTTCTCG 300
DB TACTTCCGACACCAAGCCCTCAACTTCGCTTCAAGAGATTAAGTACAGCATCTTCTCG 375
QY 301 GGGGCGTGGACACAGCAGCATTTCTGAGGTACTTTGGGGGCAACCTTGCGCTCGGC 360
DB GAGGTGTGGATCGTCATTAAGCATTTCTGCGCTTCTGCTGTAACCTTGCGCTCGGT 435
QY 361 GGTGGGCGGCGGCGACCTCCCTCTGCTTCTGTAACCCGCTGATTTTCCAGAACCCGC 420
DB GGGGCGAGCTGGGGTACTCTCTCTGCTCTGCTTCAACCTGACTTCTGAGACAG 495
QY 421 CTGGCAGCGAGCTGGGAAAGTCAGGACAGAGCGGAGATTCGAGGCGCTGGAGACTGC 480
DB CTGGCTGCGAGCTGGGAAAGTCAGGACAGAGCGGAGATTCGAGGCGCTGGAGACTGC 555
QY 481 CTGTGTGAAGATCACCAAGTCGACGAGCATCCGGGCGCTTACACAGGGCTTCAAGTCTCC 540
DB CTGTGTGAAGATCACCAAGTCGACGAGCATCCGGGCGCTTACACAGGGCTTCAAGTCTCC 615
QY 541 GTGCAAGGCGATCATATCTTACCGGGGCGCTTCTGCGGCTGTACGATTAAGGCGACGGC 600
DB GTGCAAGGCGATCATATCTTACAGAGCTGCTTACCTCGAGTCTATGACACTGCGCAAGGG 675
QY 601 ATGCTCCCCGAGCCCAAGAACAGCAGCATGCTGTGAGCTGATGATCCGCGACCGTGC 660
DB ATGCTGCCAGAGCCCAAGAAATGTGCAATATGTGAGCTGATGATGATTTGCCAGAGTGTG 735
QY 676 ATGCTGCCAGAGCCCAAGAAATGTGCAATATGTGAGCTGATGATGATTTGCCAGAGTGTG 735
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DB ACGGCGTGGCGGCGTGTCTTACCCCTTGACAGCGTGGGGGCGGCGATGATGATG 795
QY 721 CAGTCCGCGGCGCAAAAGAGCATGATGATACAGCGGACCGTGCATGTTGAGAGAG 780
DB CAGTCCGCGGCGCAAAAGAGCATGATGATGATGATGATGATGATGATGATGATG 855
QY 781 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTCAAGGGTGCAGTGCACAGCTCTCGCG 840
DB ATCTTCAGAGATGAGGGGGGCAAGGCTTCTCAAGGGTGCAGTGCACAGCTCTCGCG 915
QY 841 GGCATGAGGGGCGCTTCTGCTGCTGTGATGAGAGCTCAAGAGAGTGAATCTAA 897
DB GGCATGAGGGGCGCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATG 972

RESULT 10
US-09-811-094-2
; Sequence 2, Application US/09811094
; Patent No. US2001004414A1
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```
GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleverger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-811-094-2

Query Match      66.3%; Score 594.6; DB 9; Length 897;
Best Local Similarity 78.9%; Pred. No. 2.8e-147;
Matches 708; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 1 ATGACGGAACAGCCATCTCTTCCGCAAAAGACTTCTTGCCGAGGAGCATCCGCGCGCC 60
DB 1 ATGACGATGCCGATTTCTCTTCCGCAAAAGACTTCTTGCGAGTGAAGTGGCGGCGCC 60
QY 61 ATCTCCAGAGCGCGCTGCTCCGATCGAGCGGTCAGCTGCTGCTGAGTCCAGCAC 120
DB ATCTCCAGAGCGCGGTAGCGCCATCGAGCGGTCAGACTGCTGCTGAGTCCAGCAT 120
QY 121 GCCAGCAGCAGATGCGCGCGACAAAGCTACAAAGGCGATGCTGATCTGATTCGCC 180
DB GCCAGCAGCAGATGCTCTCTCTGAGGGGCAACCTTGCAACGCTTACCTGCG 180
QY 181 ATCCCAAGAGAGAGCGGCTGCTCTCTTCTGAGGGGCAACCTTGCAACGCTTACCTGCG 240
DB ATTCGCCAGAGAGAGATTTCTGCTCTTCTGCGCGGTAACCTTGCCATGTCATCA 240
QY 241 TACTTCCGACACCAAGCCCTCAACTTCGCTTCAAGAGATTAAGTACAGCATCTTCTCG 300
DB TACTTCCGACACCAAGCCCTTACTTCTGCTTCAAGAGATTAAGTACAGCATCTTCTCG 300
QY 301 GGGGCGTGGACAGCAGCAGCATTTCTGAGGCTTCTGCGGCAACTGGCTCGCG 360
DB GGGGCGTGGACAGCAGCAGCATTTCTGAGGCTTCTGCGGCAACTGGCTCGCG 360
QY 361 GGTGGTGTGGACAAAGAAACCCAGTTTGGCGTACTTGTGCAAGGAAATGCGCATGCGGT 360
QY 361 GGTGGTGTGGCGGCGACCTCCCTCTGCTGCTGCTGACCGCTGGATTTTTCAGAACCGCG 420
DB GGTGGTGTGGCGGCGACCTCCCTCTGCTGCTGCTGACCGCTGGATTTTTCAGAACCGCG 420
QY 421 CTGGCAGCGAGCTGGGAAAGTCAGGACAGAGCGGAGTTCGAGCGCTTGAGAGACTGC 480
DB CTGGCAGCGAGCTGGGAAAGTCAGGAGTGGAGTGAAGAGGAAATTCGAGCGCTTGAGAGACTGC 480
QY 481 CTGTGTGAAGATCACCAAGTCCAGCGCATTCGCGGCGCTGTACAGAGGCTTCACTGTCTC 540
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QY 541 GTGCAAGGCGATCATCTTACCGAGCGCGCTTCTGCGGCTGTATCATATCACTCAAGAGGA 600
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QY 601 ATGCTCCCGAGCCCAAGAACAGCAGCATGCTGTGAGTGTGATGATCCGAGACCGTGC 660
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Db 661 ACTGCTGTGCGGGTGTACTTCTATTCATTTGACACCGTTGGCGCCGCGCATGATGATG 720
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RESULT 11

US-09-810-644-2

/ Sequence 2, Application US/09810644
/ Patent No. US20020012992A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Christen M.
/ APPLICANT: Davis, Robert E.
/ APPLICANT: Clevenger, William
/ APPLICANT: Wiley, Sandra Eileen
/ APPLICANT: Willet, Scott W.
/ APPLICANT: Szabo, Tomas R.
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Moos, Walter H.
/ APPLICANT: Pel, Yezhong
/ TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
/ TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
/ FILE REFERENCE: 660088.420D3
/ CURRENT APPLICATION NUMBER: US/09/810,644
/ CURRENT FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 897
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-810-644-2

Query Match 66.3%; Score 594.6; DB 9; Length 897;
Best Local Similarity 78.9%; Pred. No. 2,8e-147;
Matches 708; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 1 ATGAGGGAACAGGCGCATCTCTCGCCAAAGACTCTTGGCGGAGGACATCGCGCGCC 60
Db 1 ATGAGAGATGGCGCATGTCTCTCGCCAAAGACTCTTGGCGGAGGAGTGAAGCGCGCGAC 60
QY 61 ATCTTCAGAGAGGGCGCTGCTGATCGAGCGGGCTCAAGGCTGCTGCGAGGTCCAGCAC 120
Db 61 ATCTTCAGAGAGGGCGGTGAGCGCCATCGAGCGGGTCAAGGCTGCTGCGAGGTCCAGCAT 120
QY 121 GCCAGCAAGCAGATCGCCCGCCGCAAGCAGATCAAGGGCATCTGACATCTATTCGCC 180
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QY 181 ATCCCAAGGAGAGGGCGGTGCTCTCTTGTGAGGGGCAACCTTGCCAAAGTCAATGCC 240
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QY 241 TACTTCCCACTCAAGGCTCACTTGGCTTCAAGAGTAAAGTCAAGCAGATCTTCTCG 300
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QY 421 CTGGCAGCGAGCTGGGAAAGTACAGCAGACAGCCGAGTTCCGAGGCTTGGAGAGACTGC 480
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QY 541 GTGCAGGAGCATCATCTTACCGGGCGCTTACCTTCCGCTGTGATGATGATGCGCAAGGCG 600
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QY 841 GGCATGGGGGGCGCTTGTGCTGTGCTGTACAGCAGCTCAAGAGGTGATCTAA 897
Db 841 GGCATGGGTGTGCTTGTGCTGTCTTGTATGATGAATCAAGAGTACACATAA 897

RESULT 12

US-09-185-904A-2

/ Sequence 2, Application US/09185904A
/ Patent No. US20020177185A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Christen M.
/ APPLICANT: Davis, Robert E.
/ APPLICANT: Clevenger, William
/ APPLICANT: Wiley, Sandra Eileen
/ APPLICANT: Willet, Scott W.
/ APPLICANT: Szabo, Tomas R.
/ APPLICANT: Ghosh, Soumitra S.
/ TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
/ TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
/ TITLE OF INVENTION: THEREFOR
/ FILE REFERENCE: 660088.420
/ CURRENT APPLICATION NUMBER: US/09/185,904A
/ CURRENT FILING DATE: 1998-11-03
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 897
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-185-904A-2

Query Match 66.3%; Score 594.6; DB 10; Length 897;
Best Local Similarity 78.9%; Pred. No. 2,8e-147;
Matches 708; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 1 ATGAGGGAACAGGCGCATCTCTCGCCAAAGACTCTTGGCGGAGGACATCGCGCGCC 60
Db 1 ATGAGAGATGGCGCATGTCTCTCGCCAAAGACTCTTGGCGGAGGAGTGAAGCGCGCGAC 60
QY 61 ATCTTCAGAGAGGGCGCTGCTGATCGAGCGGGTCAAGGCTGCTGCTGAGGTCCAGCAC 120
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QY 121 GCCAGCAAGCAGATTCGCCCGCCGCAAGCAGATCAAGGGCATCTGTGATGATGATGCTCCG 180

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:01:32 : Search time 83 Seconds
(without alignments)
569.886 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGGIAA.....LRGMCARVLYLDELKRYI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	21	AAV71033
2	1543	100.0	298	22	AAAM39641
3	1543	100.0	298	22	AAU01200
4	1543	100.0	298	22	AAU10380
5	1543	100.0	323	22	AAAM41427
6	1463	94.8	298	23	AAO18516
7	1454	94.2	298	21	AAV71032
8	1454	94.2	298	23	AAU01199
9	1454	94.2	298	23	AAU10379

10	1418	91.9	429	24	ABR41715	Human DITHP organe
11	1412	91.5	298	19	AAW61169	Anti protein. Mus
12	1406	91.1	293	22	ABU53219	Human metabolism-a
13	1385.5	89.8	297	21	AAV71031	Human adenine nucl
14	1385.5	89.8	297	22	AAU01198	Human adenine nucl
15	1385.5	89.8	297	23	AAU10378	Human adenine nucl
16	1367.5	88.6	325	22	ABG15423	Novel human diago
17	1288	83.5	263	22	ABG27056	Drosophila melanog
18	1254.5	81.3	299	22	ABG66082	Drosophila melanog
19	1254.5	81.3	299	22	ABG66082	Drosophila melanog
20	1137.5	73.7	307	22	ABU58380	Drosophila melanog
21	1119	72.5	315	22	ABU53218	Human metabolism-a
22	1119	72.5	315	23	ABE21175	Human TRICH-19 pro
23	1044	67.7	228	23	ABP74106	Human ovarian anti
24	981	63.6	222	23	ABP74106	Human TRICH SEQ ID
25	879.5	57.0	298	22	ABG18922	Novel human diago
26	788.5	51.1	301	23	ABP73357	Candida albicans e
27	763	49.4	484	22	ABG15422	Novel human diago
28	749.5	48.6	386	22	ABG27055	Novel human diago
29	743	48.2	379	24	ABP81267	ADP/ATP carrier pr
30	742.5	48.1	346	21	AAG37261	Arabidopsis thalia
31	742.5	48.1	346	21	AAG37261	Arabidopsis thalia
32	742.5	48.1	346	21	AAG37264	Arabidopsis thalia
33	742.5	48.1	346	21	AAG37264	Arabidopsis thalia
34	742.5	48.1	346	21	AAG38460	Arabidopsis thalia
35	742.5	48.1	363	21	AAG36576	Arabidopsis thalia
36	742.5	48.1	363	21	AAG37260	Arabidopsis thalia
37	742.5	48.1	373	21	AAG37263	Arabidopsis thalia
38	742.5	48.1	363	21	AAG38459	Arabidopsis thalia
39	742.5	48.1	381	21	AAG36575	Arabidopsis thalia
40	742.5	48.1	381	21	AAG37259	Arabidopsis thalia
41	742.5	48.1	381	21	AAG37262	Arabidopsis thalia
42	742.5	48.1	381	21	AAG38458	Arabidopsis thalia
43	742.5	48.1	992	21	AAG38672	Arabidopsis thalia
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ALIGNMENTS

RESULT 1	
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DT	XX
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XX	Human adenine nucleotide translocator ANT3.
DE	XX
XX	XX
KW	Human: adenine nucleotide translocator: ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotrophic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparkinson; cerebroprotective; therapeutic; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	XX
OS	XX
XX	Homo sapiens.
XX	XX
PN	XX
XX	WO200026370-A2.
PD	XX
XX	11-MAY-2000.
XX	XX
PF	XX
XX	03-NOV-1999; 99WO-0525883.
XX	XX
PR	03-NOV-1998; 98US-0185904.
XX	08-SEP-1999; 99US-0393441.
XX	XX

(MITO-) MITOKOR.

Anderson-CM, ~~David~~ RE, Clewenger W, Wiley SE, Miller SW, Szabo TR;Gosh SS; ~~David~~ RE.

WPI: 2000-365619/31.

N-PSDB: AAD00521.

Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease

Claim 46; Page 173-174; 175pp; English.

The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, hyperproliferative encephalopathy, lactic acidosis and stroke (MEAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MID), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT3 from human brain.

Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 21; Length 298;

Best Local Similarity 100.0%; Pred. No. 4, 6e-157; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVVKLLQVOHASKQIADKQYGYDCIYR 60
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DB 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVVKLLQVOHASKQIADKQYGYDCIYR 60
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DB 61 IPKEGCVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
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   121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
QY 181 VOGIIIRAAVFGVYDTAKGMLDPPKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
   181 VOGIIIRAAVFGVYDTAKGMLDPPKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKGMLDPPKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
QY 241 OSGRKADIMYTGTVDCMKRIFRDEGKAFKAGMSNVLMGAGAVLVLYDELKVI 298
   241 OSGRKADIMYTGTVDCMKRIFRDEGKAFKAGMSNVLMGAGAVLVLYDELKVI 298
DB 241 OSGRKADIMYTGTVDCMKRIFRDEGKAFKAGMSNVLMGAGAVLVLYDELKVI 298

```

RESULT 2
ID AA039641 standard; Protein; 298 AA.

AC AA039641;

22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 2786.

Human, noctropic; immunosuppressant; cytoskeletal; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

Chemokinetic; thrombolytic; drug screening; arthritis; inflammation; Leukaemia.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US34263.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.

(HXSE-) HXSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

Zhao QA, Zhou P, Goodrich R, Drmanac RT;

WPI: 2001-442253/47.

N-PSDB: AA158797.

Novel nucleic acids and polypeptides, useful for treating disorders

such as central nervous system injuries

Example 4; SEQ ID NO 2786; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA038642-AA042213), with noctropic, immunosuppressant and cytoskeletal activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemia and C.N.S. disorders.

Note: The sequence data for this patent did not form part of the printed specification.

Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 22; Length 298;

Best Local Similarity 100.0%; Pred. No. 4, 6e-157; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVVKLLQVOHASKQIADKQYGYDCIYR 60
   1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVVKLLQVOHASKQIADKQYGYDCIYR 60
DB 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVVKLLQVOHASKQIADKQYGYDCIYR 60
QY 61 IPKEGCVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
   61 IPKEGCVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
DB 61 IPKEGCVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
   121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
QY 181 VOGIIIRAAVFGVYDTAKGMLDPPKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
   181 VOGIIIRAAVFGVYDTAKGMLDPPKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKGMLDPPKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240

```


QY 241 QSGRKGADIMYGTGDCMRKIFRDEGKAFKFGAMSNVLRGGAFLVLYDELKRVY 298
 DB 241 QSGRKGADIMYGTGDCMRKIFRDEGKAFKFGAMSNVLRGGAFLVLYDELKRVY 298
 RESULT 3
 AAU01200
 ID AAU01200 standard; Protein; 298 AA.
 AC AAU01200;
 XX 07-SEP-2001 (first entry)
 DT Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS WO200132876-A2.
 PN 10-MAY-2001.
 PD 03-NOV-2000; 2000WO-US30535.
 PF 03-NOV-1999; 99US-0434354.
 PR (MITO-) MITOKOR.
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Filiger LG;
 PI Velicelcbl G, Davis RE;
 XX MPI: 2001-291054/30.
 DR N-PSDB; AAS05903.
 DR New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 XX fused to energy transfer molecule -
 XX Disclosure; Fig 2; 186pp; English.
 PS The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX Sequence 298 AA;
 SO Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFEQATSFKADFLAGGIAAISTAVAPIERVKLLQVOHASQIADKQYGIYDCIYR 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 MFEQATSFKADFLAGGIAAISTAVAPIERVKLLQVOHASQIADKQYGIYDCIYR 60
 QY 61 IPREGQVLSFMRGNLANVIRYPTQALNFAFDKQKQIPLGGVDKHTQFMRFAGNLASG 120
 DB 61 IPREGQVLSFMRGNLANVIRYPTQALNFAFDKQKQIPLGGVDKHTQFMRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLDCLVYKIRKSDGIRLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLDCLVYKIRKSDGIRLYOGFSVS 180
 QY 181 VGGITTYRAAYGVYDFAKGLPDPKNTHTIVVSMIAQVTVAVGVVSPFDTVRRRMW 240
 DB 181 VGGITTYRAAYGVYDFAKGLPDPKNTHTIVVSMIAQVTVAVGVVSPFDTVRRRMW 240
 QY 241 QSGRKGADIMYGTGDCMRKIFRDEGKAFKFGAMSNVLRGGAFLVLYDELKRVY 298
 DB 241 QSGRKGADIMYGTGDCMRKIFRDEGKAFKFGAMSNVLRGGAFLVLYDELKRVY 298
 RESULT 4
 AAU10380
 ID AAU10380 standard; Protein; 298 AA.
 AC AAU10380;
 XX 14-FEB-2002 (first entry)
 DT Human adenine nucleotide translocator 3 (ANT3).
 DE Human; adenine nucleotide translocator; ANT;
 KM mitochondrial matrix protein.
 XX Homo sapiens.
 OS WO200185944-A2.
 PN 15-NOV-2001.
 PD 11-MAY-2001; 2001WO-US15416.
 PF 11-MAY-2000; 2000US-0569327.
 PR (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 XX MPI: 2002-055598/07.
 DR N-PSDB; AAS16690.
 DR Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX Example 3; Fig 2; 147pp; English.
 PS The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.

XX Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTEGALISFAKDFLAGGIAAISKTAFAPIERVKLLQVHASKQIADKQKGYDCIYR 60
 1 MTEGALISFAKDFLAGGIAAISKTAFAPIERVKLLQVHASKQIADKQKGYDCIYR 60
 61 IPKDGVLSEFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAG 120
 61 IPKDGVLSEFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAG 120
 121 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVKTIKSDGIRGLYOGFSVS 180
 121 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVKTIKSDGIRGLYOGFSVS 180
 181 VGGIIRAAVFGVDTAKGMLDPKNTHTIVSWMIAQVTAAGVSYPEDTVRRMM 240
 181 VGGIIRAAVFGVDTAKGMLDPKNTHTIVSWMIAQVTAAGVSYPEDTVRRMM 240
 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGKGAFVLYLDELKVI 298
 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGKGAFVLYLDELKVI 298

RESULT 5
 ID AAM41427 standard; Protein: 323 AA.

AC AAM41427;
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 6358.
 XX Human; nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia.
 XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 PD 26-DEC-2000; 2000WO-US34263.
 PF 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0634510.
 PR 14-SEP-2000; 2000US-0662391.
 PR 19-OCT-2000; 2000US-0683036.
 PR 23-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AU, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR N-PSDB: AA160583.
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 such as central nervous system injuries -

XX Example 2; SEQ ID NO 6358; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nocitropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 323 AA:

Query Match 100.0%; Score 1543; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 5,2e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTEGALISFAKDFLAGGIAAISKTAFAPIERVKLLQVHASKQIADKQKGYDCIYR 60
 26 MTEGALISFAKDFLAGGIAAISKTAFAPIERVKLLQVHASKQIADKQKGYDCIYR 85
 61 IPKDGVLSEFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAG 120
 86 IPKDGVLSEFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAG 145
 121 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVKTIKSDGIRGLYOGFSVS 180
 146 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVKTIKSDGIRGLYOGFSVS 205
 181 VGGIIRAAVFGVDTAKGMLDPKNTHTIVSWMIAQVTAAGVSYPEDTVRRMM 240
 206 VGGIIRAAVFGVDTAKGMLDPKNTHTIVSWMIAQVTAAGVSYPEDTVRRMM 265
 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGKGAFVLYLDELKVI 298
 266 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGKGAFVLYLDELKVI 323

RESULT 6
 ID AAO18516 standard; Protein: 298 AA.

AC AAO18516;
 DT 11-OCT-2002 (first entry)
 DE Human insulin receptor signaling modifier SEQ ID NO: 54.
 XX Human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic.
 XX Homo sapiens.
 OS WO200255664-A2.
 PN 18-JUL-2002.
 PD 11-JAN-2002; 2002WO-US01048.
 PF 12-JAN-2001; 2001US-261226P.
 PR 12-JAN-2001; 2001US-261303P.
 PR 12-JAN-2001; 2001US-261304P.
 PR 12-JAN-2001; 2001US-261335P.
 PR 12-JAN-2001; 2001US-261336P.

PR 12-JAN-2001; 2001US-261361P.
PR 12-JAN-2001; 2001US-261456P.
PR 12-JAN-2001; 2001US-261457P.
PR 12-JAN-2001; 2001US-261458P.
PR 12-JAN-2001; 2001US-261459P.
PR 12-JAN-2001; 2001US-261461P.
PR 12-JAN-2001; 2001US-261518P.
PR 12-JAN-2001; 2001US-261531P.
PR 12-JAN-2001; 2001US-261532P.
PR 12-JAN-2001; 2001US-261589P.
PR 12-JAN-2001; 2001US-261590P.
PR 12-JAN-2001; 2001US-261694P.
PR 12-JAN-2001; 2001US-261695P.
PR 12-JAN-2001; 2001US-261697P.
XX (EXEL-) EXELIXIS INC.
XX
PI Seidel-Dugan C, Ferguson KC, Kidd T;
XX
XX WPI; 2002-599664/64.
DR N-PSDB; AAL48635.
XX
XX
PT Identifying an insulin receptor signaling modulator, useful as drug
PT targets for treating diabetes or metabolic disorders, comprises
PT contacting an assay system comprising insulin receptor signaling
PT modifiers with a test agent
XX
XX
PS Disclosure; Page 160-161; 232pp; English.
XX
XX
CC The present invention relates to a method of identifying a candidate
CC Insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.
XX
XX
SQ Sequence 298 AA;
Query Match 94.8%; Score 1463; DB 23; Length 298;
Best Local Similarity 92.9%; Pred. No. 1.8e-148;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTEQAIISPAKDLFLAGIAAISKTAAPLIERVKLLQVOHASKQIADKQYKGIIVDCIYR 60
DB 1 MTDAAISPAKDLFLAGIAAISKTAAPLIERVKLLQVOHASKQIADKQYKGIIVDCIYR 60
QY 61 IPEQGVLSFWKGNLANVIRFPTQALNFAFKKQYKQIFLGVDKHTQWRFRAGNLASG 120
DB 61 IPEQGVLSFWKGNLANVIRFPTQALNFAFKKQYKQIFLGVDKHTQWRFRAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADYVGSSTEREFRIGDCLVYITKSDGIRGLYGFSSYS 180
DB 121 GAAGATSLCFVYPLDFARTLADYVGSSTEREFRIGDCLVYITKSDGIRGLYGFSSYS 180
QY 122 GAAGATSLCFVYPLDFARTLADYVGSSTEREFRIGDCLVYITKSDGIRGLYGFSSYS 180
DB 122 GAAGATSLCFVYPLDFARTLADYVGSSTEREFRIGDCLVYITKSDGIRGLYGFSSYS 180
QY 181 VOGIILYRAAYEGVYDTAKGMLDPKNTNTHIVSWMTAQVTYAVAGVVSYPEDTVRRMM 240
DB 181 VOGIILYRAAYEGVYDTAKGMLDPKNTNTHIVSWMTAQVTYAVAGVVSYPEDTVRRMM 240
QY 241 QSGRKADIMYTGTCVCMKRIFDEBGAFAFKKANSNVLRGKMGAVLYLYDELAK 296
DB 241 QSGRKADIMYTGTCVCMKRIFDEBGAFAFKKANSNVLRGKMGAVLYLYDELAK 296
RESULT 7
AAV71032 standard; Protein; 298 AA.

XX
AC AAV71032;
XX
XX 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT2.
XX
XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
XX mitochondrial permeability transition; neuroprotective; neurotropic;
XX antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
XX antipariatic; cerebroprotective; therapeutic; screening; psoriasis;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
XX mitochondrial diabetes and deafness; hyperproliferative disorder;
XX myoclonic epilepsy red ragged fibre syndrome.
XX
XX Homo sapiens.
XX
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1998; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS;
XX
XX WPI; 2000-365619/31.
DR N-PSDB; AAD00520.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
XX
XX Claim 45; Page 172-173; 175pp; English.
PS
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.
XX
XX
SQ Sequence 298 AA;
Query Match 94.2%; Score 1454; DB 21; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MTEQAIISPAKDLFLAGIAAISKTAAPLIERVKLLQVOHASKQIADKQYKGIIVDCIYR 60
DB 1 MTDAAISPAKDLFLAGIAAISKTAAPLIERVKLLQVOHASKQIADKQYKGIIVDCIYR 60
QY 61 IPEQGVLSFWKGNLANVIRFPTQALNFAFKKQYKQIFLGVDKHTQWRFRAGNLASG 120
DB 61 IPEQGVLSFWKGNLANVIRFPTQALNFAFKKQYKQIFLGVDKHTQWRFRAGNLASG 120

Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGIGDCLVKITKSDGIRGLYOGFSYS 180
Db 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGIGDCLVKITKSDGIRGLYOGFSYS 180
QY 181 VGGIITRYAAVFGYVDYAKGMLPDKNTHIVSWMIAGVTAVAGVSYEPDVRRRMM 240
Db 181 VGGIITRYAAVFGYVDYAKGMLPDKNTHIVSWMIAGVTAVAGVSYEPDVRRRMM 240
QY 241 QSGRKGADIMYTGTDVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLVDLKK 296
Db 241 QSGRKGADIMYTGTDVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLVDLKK 296

RESULT 8

AAU01199 standard; Protein: 298 AA.

AC AAU01199;

DX 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

KM Human: adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;

KM mitochondrial permeability transition pore component; cell survival;

KM mitochondrial core component; mitochondrial related disorder; cancer;

KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN W0200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US0535.

PR 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Willey SE, Andreyev AY, Frigeri LG;

PI Vellcellebl G, Davis RE;

DR N-PSDB; AAS05902.

PT New nucleic acid expression constructs, useful for screening for agents

PT that alter mitochondrial permeability transition (MPT), comprises

PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide

PT fused to energy transfer molecule -

PS Disclosure: Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-2

CC (ANT-2) protein. ANT proteins are mitochondrial permeability

CC transition (MPT) pore components responsible for mediating transport

CC of ADP across the mitochondrial inner membrane. ANT proteins interact

CC with other mitochondrial core components e.g. cyclophilins to

CC regulate MPT. The present invention relates to a novel nucleic acid

CC expression construct comprising a promoter operably linked to a

CC polynucleotide encoding a mitochondrial pore component polypeptide

CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein

CC expression construct can alter mitochondrial membrane permeability

CC transition and/or alter the interaction between mitochondrial core

CC components. The methods are useful for screening for agents that alter

CC MPT and/or cell survival. These agents are useful for the prevention or

CC treatment of diseases associated with altered mitochondrial function or

CC dysfunctional cell survival, such as Alzheimer's disease, diabetes

CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,

CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 298 AA;

SQ Query Match 94.2%; Score 1454; DB 22; Length 298;

Best Local Similarity 92.6%; Pred. No. 1.7e-147;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQALISFAPDLAGGIAAISKTAFAPIERVKLLQVOHASKQIAADKQYKGVDCIVR 60

Db 1 MTEQALISFAPDLAGGIAAISKTAFAPIERVKLLQVOHASKQIAADKQYKGVDCIVR 60

QY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120

Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGIGDCLVKITKSDGIRGLYOGFSYS 180

Db 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGIGDCLVKITKSDGIRGLYOGFSYS 180

QY 181 VGGIITRYAAVFGYVDYAKGMLPDKNTHIVSWMIAGVTAVAGVSYEPDVRRRMM 240

Db 181 VGGIITRYAAVFGYVDYAKGMLPDKNTHIVSWMIAGVTAVAGVSYEPDVRRRMM 240

QY 241 QSGRKGADIMYTGTDVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLVDLKK 296

Db 241 QSGRKGADIMYTGTDVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLVDLKK 296

RESULT 9

AAU10379 standard; Protein: 298 AA.

AC AAU10379;

DX 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).

KM Human: adenine nucleotide translocator; ANT; ss;

KM mitochondrial matrix protein.

OS Homo sapiens.

PN W0200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001MO-US15416.

PR 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SW, Szabo TR;

PI Ghosh SS, Moos WH, Pel Y, Carroll AK;

DR N-PSDB; AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide

PT translocator polypeptides, comprises a regulated promoter linked to

PT nucleic acid encoding the polypeptide -

PS Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (1)

CC comprising a regulated promoter operably linked to a nucleic acid

CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT

CC proteins mediate the exchange of ADP synthesized in the mitochondrial

CC matrix for ADP in the cytosol. (1) is useful for producing recombinant

CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and

CC culturing the host cell. (1) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT2.
XX

SO Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 23; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSFARKDFLAGIAAISTKTAVERVLLQVGHASQIADKQKIVDCIYR 60
DB 1 MTDALISFARKDFLAGVAAIAISTKTAVERVLLQVGHASQIADKQKIVDCIYR 60

QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAG 120

QY 121 GAAGATSLCFVYPLDFAFRRLADVKSGTEREFGDGLVKTTSDDIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDFAFRRLADVKSGTEREFGDGLVKTTSDDIRGLYQGFVS 180

QY 181 VQGIITIRRAAFGVYDTAKGMLPDKNTHIVVSMIAQVTVAVAGVSYPTDVRRRMM 240
DB 181 VQGIITIRRAAFGVYDTAKGMLPDKNTHIVVSMIAQVTVAVAGVSYPTDVRRRMM 240

QY 241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLKMGCAFVLYDELKR 296
DB 241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLKMGCAFVLYDELKR 296

RESULT 10
ABR41715
ID ABR41715 standard; Protein; 429 AA.
XX
XX ABR41715;
D7 02-JUN-2003 (first entry)
XX
XX Human DITHP organelle-associated protein.
XX
XX Human: dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW organelle-associated protein.
XX
XX Homo sapiens.
OS
PN WO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US10056.
XX
PR 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 16-MAY-2001; 2001US-280068P.
PR 17-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 19-JUN-2001; 2001US-291849P.
PR 20-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Daifio A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstlin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
XX WPI: 2003-129518/12.
DR N-PDB: ACC46652.
XX
XX Novel human diagnostic and therapeutic polypeptide useful for
PT identifying test compound which specifically binds to a polypeptide
PT encoded by human diagnostic and therapeutic polynucleotide, and to
PT induce antibodies -
XX
XX Claim 27; SEQ ID No 1250; 591pp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
CC encoded proteins (DITHP: ABR41136-ABR41812). The invention also relates
CC to polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods
CC of detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which is an organelle-
CC associated protein.
CC Note: The sequence data for this patent did not form part of the WPIPO
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX
XX Sequence 429 AA;

Query Match 91.9%; Score 1418; DB 24; Length 429;
Best Local Similarity 95.2%; Pred. No. 2e-143;
Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;

QY 1 MTEQATSFARKDFLAGIAAISTKTAVERVLLQVGHASQIADKQKIVDCIYR 60
DB 26 MTEQATSFARKDFLAGIAAISTKTAVERVLLQVGHASQIADKQKIVDCIYR 85

QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAG 145

QY 121 GAAGATSLCFVYPLDFAFRRLADVKSGTEREFGDGLVKTTSDDIRGLYQGFVS 180
DB 146 GAAGATSLCFVYPLDFAFRRLADVKSGTEREFGDGLVKTTSDDIRGLYQGFVS 205

QY 181 VQGIITIRRAAFGVYDTAKGMLPDKNTHIVVSMIAQVTVAVAGVSYPTDVRRRMM 240
DB 206 VQGIITIRRAAFGVYDTAKGMLPDKNTHIVVSMIAQVTVAVAGVSYPTDVRRRMM 265

Oy		241	OSGRGGADIMYTGTCCMKIRIDGCGAFAFKGA-W-----SNVTRMGKA	285
Dd		266	OSRGAGADIYMTGTVDCKMRIFRDEGCAPKFGSHWKQNTLDALEGSFSA	316
Db				
	RESULT 11			
ID	AAM61169			
Xx	AAM61169 standard; Protein; 298 AA.			
Xx	AAM61169;			
Xx	AAW61169;			
Xx	28-SEP-1998 (first entry)			
De	Anrl protein.			
Kw	Anrl; Adenine nucleotide translocator; cloning; screening;			
Km	DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;			
Rv	kprob; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;			
Km	hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;			
Kw	lactic acidosis; degenerative muscle disease.			
Xx	Mus sp.			
Xx	MO9819714-AI.			
Pn	XX XX XX XX XX XX XX			
Pd	14-MAY-1998.			
Pf	31-OCT-1997; 97WO-US19882.			
Px	01-NOV-1996; 96US-0030017.			
Pr	(UYEM-) UNIV EMORY.			
Pa	Graham BC, Macgregor GR, Wallace DC;			
Pt	WPJ: 1998-286608/25.			
Dr	N-PADB: AAV36479.			
Dc	Mouse lacking heart-muscle adenine nucleotide translocator protein - useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or gene therapies			
Pt	Disclosure; Page 39-40; 61pp; English.			
Pt	The present sequence is the mouse Anrl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Anrl cDNA as a probe. The Anrl cDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Anrl protein is encoded by CC CCG Tgg diodeoxy terminaler cycle sequencing. This protein is located at the Anrl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Anrl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Anrl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypotrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/moderate ATP and ADP exchange across the mitochondrial membrane independent of ANTL.			
Cc	Increase/moderate ATP and ADP exchange across the mitochondrial membrane independent of ANTL.			
Cc	Independent of ANTL.			
Cc	Sequence 298 AA:			
Sq	Query Match 91.5%; Score 1412; DB 19; Length 298; Best Local Similarity 88.0%; Pred. No. 5.4e-143; Matches 19; Conservative 19; Mismatches 15; Indels 0; Gaps 0			
Oy	1 MTBOAISFANDFLAGIAAIATKTANVAIERVKLLIQVOHASKOITADOKYGINDCYR	60		
Db	1 MGDDALSFLLDPLFLAGIIANAASKVTAIEERVKLLAQVOHASKOISAKROKGILDCVRA	60		
Oy	61 IPKEGVLSFWRCNLNAVRIFFPTDALNPAFKDKYQDFLGSGVDNRHTOFMYRFEGNIASG	120		
Db	61 IPRDGGLTSWRKRNLNAVRIFFPTDALNPAFKDKYQDFLGSGVDNRHKOFMRYEFGNISIGS	120		

QY	121	GAAGAGTSTSCFVYPLDPARTRLAADVGKGTGEREPRRGIDGLVYTRKSGINGLYQGSFVS	180
Db	121	GAAGAGTSTSCFVYPLDPARTRTLAADVGKSGSREBNIGDGLTRFKRSDINGLYQGSFVS	180
QY	181	VGGITTYRAAYFVGYYTAKGMLPDKRNTHIYVSMIAQOTYANAGVASYPDDYRRRMM	240
Db	181	VGGITTYRAAYFVGYYTAKGMLPDKRNTHIIVSMIAQSTAYAGLVSPDDYRRRMM	240
QY	241	QSGRGAGDIWYTGTVDCWKRIFRDSGGRAPFKGAMSVLVLMGMCAGVALVLDLKKYV	298
Db	241	QSGRGAGDIWYTGTVDCWKRIRKIDEGANAFPKGAMSVLVLMGMCAGVALVLDLKKYV	298
RESULT 12			
AB053219	ID	AB053219 standard; Protein; 293 AA.	
AC	AB053219;		
AD	14-APR-2003	(first entry)	
DE	Human metabolism-associated DKFZptases3_35n12 homologue #1.		
DE	Human; gene therapy; vaccine; disease treatment; detection.		
OS	Homo sapiens.		
XX	WO200112659-A2.		
XX	22-FEB-2001.		
PF	18-AUG-2000; 2000MO-IB01496.		
PR	18-AUG-1999; 99US-0149499.		
PR	28-SEP-1999; 99US-0156503.		
XX	(GEHU-) GERMAN HUMAN GENOME PROJECT.		
XX	Wiemann S;		
PI	WPI: 2001-327840/34.		
PT	Nucleic acids having the sequences of clones isolated from libraries of		
XX	different human tissues, useful in recombinant DNA methodologies -		
PS	Example III; Page 850; 1095pp; English.		
CC	This invention describes novel polynucleotides and polypeptides isolated		
CC	from human cDNA libraries which can be used for gene therapy or in		
CC	vaccines. The polynucleotides of the invention and antibodies encoded by		
CC	them may be used in the prevention, diagnosis and treatment of diseases		
CC	associated with inappropriate polypeptide expression. The products of the		
CC	invention may also be used to identify modulators of expression and		
CC	activity and to down regulate expression and activity. The antibodies of		
CC	the invention may also be used as diagnostic agents for detecting the		
CC	presence of polypeptides in samples. This sequence represents a homologue		
CC	of a polypeptide described in the disclosure of the invention.		
XX			
XX	Sequence 293 AA:		
QY	Query Match	91.1%; Score 1406; DB 22; Length 293;	
Db	Best Local Similarity	90.1%; Pred. No. 2.3e-142;	
	Matches 203; Conservative 17; Mismatches 12; Indels 0; Gaps 0		
QY	5 AISRKDFLAGGTAIAISTAVAPLERKLLQVQASKQIAADKQYGYDCVIRIPKE	64	
Db	1 ALSTFKDPLAGGTAIAASTAVAPLERKLLQVQASKQISLEKQYGGIIDCVIRIPKE	60	
QY	65 QGVLSFVRGNLANVIRFPTQALNFAFKDKTKQLETGVDYDKRFTQFMRRYPAGNLASGAG	124	
Db	61 QGVLSFVRGNLANVIRFPTQALNFAFKDKTKQLETGVDYDKRQFMRRYPAGNLASGAG	120	

QY 125 ATSLCPVYPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVSGI 184
 Db 121 ATSLCPVYPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVSGI 180
 QY 185 IYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVYSPEDVRRRRMMQSGR 244
 Db 181 IYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVYSPEDVRRRRMMQSGR 240
 QY 245 KQADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLRGNGAFVLYLDELKR 296
 Db 241 KQADIMYTGTVDCMKRIRKADGKAFKFGKAMSNVLRGNGAFVLYLDELKR 292

RESULT 13
 AAY71031
 ID AAY71031 standard; Protein; 297 AA.
 XX AAY71031;
 AC AAY71031;
 XX 29-ADG-2000 (first entry)
 DT
 XX Human adenine nucleotide translocator ANTL.
 DE
 XX Human: adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; neurotrophic;
 KM antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KM antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 KW
 XX Homo sapiens.
 OS
 XX WO200026370-A2.
 PN
 XX 11-MAY-2000.
 PD
 XX 03-NOV-1999; 99WO-US25883.
 PF
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 XX (MITO-) MITOKOR.
 PA
 XX Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
 PI Ghosh SS;
 DR MPI; 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PT
 XX Claim 44; Page 172; 175pp; English.
 PS
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, MELAS, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIND), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANTL from human brain.
 XX

SO Sequence 297 AA;
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAIISFAKDLFLAGIAAISTKTAAPTEERKLLIQVOHASKQIAADKQYGIYDCIVR 60
 Db 1 MGDHAKSEFLKDLFLAGIAAASVSKTAPTEERKLLIQVOHASKQISAEQYGIIDCYVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGGVDVHTQFRRFAGNLASG 120
 Db 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGGVDVHTQFRRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFAFRRLADVGRR-AQREFHGLGDCIIRKIFKSDGLRGLYOGFNV 179
 QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVYSPEDVRRRRMM 240
 Db 180 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGLSTPEVRRRRMM 239
 QY 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLRGNGAFVLYLDELKRV 298
 Db 240 QSGRKADIMYTGTVDCMKRIKADGKAFKFGKAMSNVLRGNGAFVLYLDELKRV 297

RESULT 14
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX AAU01198;
 AC AAU01198;
 XX 07-SEP-2001 (first entry)
 DT
 XX Human adenine nucleotide translocator-1 (ANT-1) protein.
 DE
 XX Human: adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 KW
 XX Homo sapiens.
 OS
 XX WO200132876-A2.
 PN
 XX 10-MAY-2001.
 PD
 XX 03-NOV-2000; 2000WO-US30535.
 PF
 XX 03-NOV-1999; 99US-0434354.
 PR
 XX (MITO-) MITOKOR.
 PA
 XX Murphy AN, Clevenger W, Willey SE, Andreyev AV, Fritger LG;
 PI Vellelebi G, Davis RE;
 DR MPI; 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PT
 XX Disclosure; Fig 2; 166pp; English.
 PS
 XX The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability

CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 22; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQAISFANDFLAGIAAISTAVAPIERYKLLLOVHASKOIADKOYGIYDCYR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERYKLLLOVHASKOIADKOYGIYDCYR 60
 QY 61 IPKGGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRFRAGNLASG 120
 DB 61 IPKGGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRFRAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFAFRTLAADVGRS-TEREPRGLGDCLVKTKSDGIRGLYOGFSYS 180
 DB 121 GAAGATSLCFYVPLDFAFRTLAADVGRS-AGEHFGHGLGDCIKIKFSDDGIRGLYOGFSYS 179
 QY 181 VGGIIIRAAFYGYVDFAKGMPLDPKNTHTIVSMIAQVTAAGVSVPEFVRRRMM 240
 DB 180 VGGIIIRAAFYGYVDFAKGMPLDPKNTHTIVSMIAQVTAAGVSVPEFVRRRMM 239
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFFKGAWSNVLKMGGAFLVLYDELKVI 298
 DB 240 QSGRKGADIMYTGTVDCWKRIADGAKAFFKGAWSNVLKMGGAFLVLYDELKVI 297

RESULT 15

AAU10378 standard; Protein: 297 AA.

XX AAU10378;

XX 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 1 (ANT1).

XX Human: adenine nucleotide translocator; ANT;

XX mitochondrial matrix protein.

XX Homo sapiens.

XX MO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001MO-US15416.

XX 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;

DR NPI: 2002-055598/07.

DR N-PSDB; AASI6688.

XX Novel recombinant expression construct for producing adenine nucleotide
 XX translocator polypeptides; comprises a regulated promoter linked to
 XX nucleic acid encoding the polypeptide

XX Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT1.

SO Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 23; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQAISFANDFLAGIAAISTAVAPIERYKLLLOVHASKOIADKOYGIYDCYR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERYKLLLOVHASKOIADKOYGIYDCYR 60
 QY 61 IPKGGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRFRAGNLASG 120
 DB 61 IPKGGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRFRAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFAFRTLAADVGRS-TEREPRGLGDCLVKTKSDGIRGLYOGFSYS 180
 DB 121 GAAGATSLCFYVPLDFAFRTLAADVGRS-AGEHFGHGLGDCIKIKFSDDGIRGLYOGFSYS 179
 QY 181 VGGIIIRAAFYGYVDFAKGMPLDPKNTHTIVSMIAQVTAAGVSVPEFVRRRMM 240
 DB 180 VGGIIIRAAFYGYVDFAKGMPLDPKNTHTIVSMIAQVTAAGVSVPEFVRRRMM 239
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFFKGAWSNVLKMGGAFLVLYDELKVI 298
 DB 240 QSGRKGADIMYTGTVDCWKRIADGAKAFFKGAWSNVLKMGGAFLVLYDELKVI 297

Search completed: August 18, 2003, 16:11:32
 Job time : 85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:09:02 ; Search time 42 Seconds
(without alignments)
682.340 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEOALSFKADFLAGGIAA.....LNGMGAFVLYIDEIKKYI 298

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	1 S03894	ADP, ATP carrier pr
2	1512	98.0	298	2 B43646	ADP, ATP carrier pr
3	1454	94.2	298	1 A29132	ADP, ATP carrier pr
4	1424	92.3	298	2 T60173	adenine nucleotide
5	1422	92.2	298	1 XWBO	ADP, ATP carrier pr
6	1418	91.9	298	2 S37210	ADP, ATP carrier pr
7	1409	91.3	298	1 A44778	ADP, ATP carrier pr
8	1405	91.1	298	2 S31814	ADP, ATP carrier pr
9	1184	76.7	301	1 S31935	ADP, ATP carrier pr
10	1041	67.5	313	2 T23207	hypothetical prote
11	1039	67.3	313	2 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP, ATP carrier pr
15	943	61.1	301	2 S51132	ADP, ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP, ATP carrier pr
17	772	50.0	308	1 S30259	ADP, ATP carrier pr
18	769	49.8	322	2 T40526	ADP, ATP carrier pr
19	768	49.8	386	2 T09709	ADP, ATP carrier pr
20	766	49.6	313	1 XWMC	ADP, ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP, ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP, ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14876	ADP, ATP carrier pr
26	748	48.5	386	2 S21974	ADP, ATP carrier pr
27	747	48.4	306	2 T42011	ADP, ATP carrier pr
28	747	48.4	386	2 S17917	ADP, ATP carrier pr
29	744	48.2	387	2 S16586	ADP, ATP carrier pr

30	743	48.2	379	2 T04608	ADP, ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP, ATP carrier pr
32	742	48.1	382	2 S33630	ADP, ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP, ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP, ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP, ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP, ATP translocas
38	383	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	mitochondrial solu
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.5	475	2 T50686	peroxisomal Ca-dep
44	363	23.5	448	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

ADP, ATP carrier protein T3 - human
N/Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP,
C/Species: Homo sapiens (man)
C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C/Accession: S03894; B28116
R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.

T. Mol. Biol. 206, 261-280, 1989.

A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP

A/Reference number: S03893; MUID:89236396; PMID:2541251

A/Accession: S03894

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-298 <COZ>

R/Houlsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1

A/Reference number: A94197; MUID:88124845; PMID:2829183

A/Accession: B28116

A/Molecule type: mRNA

A/Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>

A/Cross-references: GB:003592; NID:9339722; PIDN:AAA6750.1; PID:9339723

A/Experimental source: liver

C/Genetics:

A/Gene: GDB:AMT3; AMT3Y

A/Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A/Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A/Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and G

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

F:2-298/Product: ADP, ATP carrier protein #status predicted <MAT>

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 100.0%; Score 1543; DB 1; Length 298;

Mismatches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEOALSFKADFLAGGIAAISKTAIVPIERVLLQLQVHASKQIADKQYGVDCIVR	60
DB	1	MTEOALSFKADFLAGGIAAISKTAIVPIERVLLQLQVHASKQIADKQYGVDCIVR	60
QY	61	IPKEQGLVSRKRNLANVITFPQALNFKFKYKQIFLGVDKHTQFRRYRAGNLASG	120
DB	61	IPKEQGLVSRKRNLANVITFPQALNFKFKYKQIFLGVDKHTQFRRYRAGNLASG	120
QY	121	GAAGATSLCFVYPLDFARTRLADVKGSGEREFRGLDCLVTKTSKDGIRGLYOGFSSV	180
DB	121	GAAGATSLCFVYPLDFARTRLADVKGSGEREFRGLDCLVTKTSKDGIRGLYOGFSSV	180

OY 181 VGGIIIRAAFEVYDTAKMLDPKNTHTIVSMIACTVAVAGVSYFEDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFEVYDTAKMLDPKNTHTIVSMIACTVAVAGVSYFEDTVRRMM 240
 OY 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKVI 298
 |||
 Db 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKVI 298

RESULT 2

ADP/ATP carrier protein T2 - bovine
 A:Accession: B43646
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 R:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 BiochemJ 281: 865-873, 1999
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: Preliminary
 A:Molecule type: mRNA

A:Residues: 1-298 <PDB>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 98.08; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.78; Pred. No. 3.3e-126;
 Matches 291; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 1 MTEQAISFANDFLAGIAAIAISKTAAVPIERVKLLQVOHASKQIADKQKIVDCIVR 60
 |||
 Db 1 MTEQAISFANDFLAGIAAIAISKTAAVPIERVKLLQVOHASKQIADKQKIVDCIVR 60
 OY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 |||
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFARTRLADVDGKSGTEREFGGLDCLVTKTSKDSGIRGLYQGFNS 180
 |||
 Db 121 GAAGATSLCFYVPLDFARTRLADVDGKSGTEREFGGLDCLVTKTSKDSGIRGLYQGFNS 180
 OY 181 VGGIIIRAAFEVYDTAKMLDPKNTHTIVSMIACTVAVAGVSYFEDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFEVYDTAKMLDPKNTHTIVSMIACTVAVAGVSYFEDTVRRMM 240
 OY 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKVI 298
 |||
 Db 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKVI 298

RESULT 3

ADP/ATP carrier protein T2 - human
 A:Accession: A29132
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Battni, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262: 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132
 A:Molecule type: mRNA

A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:9179246; PIDN:AAA35579.1; PID:9179247
 R:Houseworth, J.; Ataragi, C.
 Proc. Natl. Acad. Sci. U.S.A. 85: 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829383
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:9339720; PIDN:AAA36749.1; PID:9339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2P1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-q26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 94.28; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.08; Pred. No. 4.5e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQAISFANDFLAGIAAIAISKTAAVPIERVKLLQVOHASKQIADKQKIVDCIVR 60
 |||
 Db 1 MTEQAISFANDFLAGIAAIAISKTAAVPIERVKLLQVOHASKQIADKQKIVDCIVR 60
 OY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 |||
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFARTRLADVDGKSGTEREFGGLDCLVTKTSKDSGIRGLYQGFNS 180
 |||
 Db 121 GAAGATSLCFYVPLDFARTRLADVDGKSGTEREFGGLDCLVTKTSKDSGIRGLYQGFNS 180
 OY 181 VGGIIIRAAFEVYDTAKMLDPKNTHTIVSMIACTVAVAGVSYFEDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFEVYDTAKMLDPKNTHTIVSMIACTVAVAGVSYFEDTVRRMM 240
 OY 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKVI 298
 |||
 Db 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKVI 298

RESULT 4

adenine nucleotide translocator - rat
 A:Accession: I60173
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173
 R:Shiohara, T.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152: 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MUID:94002161; PMID:8399300
 A:Accession: I60173
 A:Status: Preliminary; translated from GB/EMBL/DDB

A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427
 C:Genetics:
 A:Gene: anti
 A:Intons: 37/3; 200/1; 247/1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 92.38; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.68; Pred. No. 2e-116;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY 1 MTEQAISFANDFLAGIAAIAISKTAAVPIERVKLLQVOHASKQIADKQKIVDCIVR 60
 |||
 Db 1 MTEQAISFANDFLAGIAAIAISKTAAVPIERVKLLQVOHASKQIADKQKIVDCIVR 60

QY 61 IPKQGLSLFWKGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQEMRRYFAGNLASG 120
 Db 61 IPKQGLSLFWKGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQEMRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLRADLVGKSGTEREERGLDCLVITKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFAFRTLRADLVGKSGTEREERGLDCLVITKSDGIRGLYOGFSVS 180
 QY 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVSYPEFTVRRMM 240
 Db 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVSYPEFTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIKIFDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298
 Db 241 QSGRKADIMYTGTVDCMKRIKIFDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298

RESULT 5

XMB0
 ADP,ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.U.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <PDB>
 A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
 R:Rasmussen, U.B.; Wohlrab, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:86295775; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Misra, D.; Enlitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AOU>
 A:Note: residue 52 may be methyllysine
 R:Bebel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Maasson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3H)7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:9512058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63;154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochond
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;
 Best Local Similarity 89.3%; Pred. No. 3, 1e-118;
 Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQALSFANDFLAGIAAISKTAAPVIERVKLLQVQHASQIADAKQYGIQDCTVR 60
 Db 1 MGDQALSFLEDFLAGIAAIVSKTAVPIERVKLLQVQHASQISAEKQYGIQDCTVR 60
 QY 61 IPKQGLSLFWKGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQEMRRYFAGNLASG 120
 Db 61 IPKQGLSLFWKGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQEMRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLRADLVGKSGTEREERGLDCLVITKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFAFRTLRADLVGKSGTEREERGLDCLVITKSDGIRGLYOGFSVS 180
 QY 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVSYPEFTVRRMM 240
 Db 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVSYPEFTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIKIFDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298
 Db 241 QSGRKADIMYTGTVDCMKRIKIFDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298

RESULT 6

S37210
 ADP,ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 R:Laplace, C.; Costet, P.
 submitted to the EMBL data library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <LAP>
 A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
 C:Genetics:
 A:Gene: ANCL
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.9%; Score 1418; DB 2; Length 298;
 Best Local Similarity 88.9%; Pred. No. 6, 9e-118;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQALSFANDFLAGIAAISKTAAPVIERVKLLQVQHASQIADAKQYGIQDCTVR 60
 Db 1 MGDQALSFLEDFLAGIAAIVSKTAVPIERVKLLQVQHASQISAEKQYGIQDCTVR 60
 QY 61 IPKQGLSLFWKGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQEMRRYFAGNLASG 120
 Db 61 IPKQGLSLFWKGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQEMRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLRADLVGKSGTEREERGLDCLVITKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFAFRTLRADLVGKSGTEREERGLDCLVITKSDGIRGLYOGFSVS 180
 QY 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVSYPEFTVRRMM 240
 Db 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTVAVAGVSYPEFTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIKIFDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298
 Db 241 QSGRKADIMYTGTVDCMKRIKIFDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298


```
QY      8  FAKDFLAGGIAAIAISKTAVAPIERVKLLQOVHASKQIADKQKGYDCIARIPKQGV 67
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      12  FLIDLASGGTAATAVSKTAIVAPIERVKLLQOVDAKALAVKRYKIMDLIRPKQGV 71
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      68  LSFWRGNLANVIRYEPFOALNFAFKDKYKQIFLGVDKHTQWRFRFAGNLASGAGAT 127
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      72  AALMRGNLANVIRYEPFOALNFAFKDKYKQIFLGVDKHTQWRFRFAGNLASGAGAT 131
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      128  LCFVYPLDFARTRLAADVGSCTEREERGLGDLVITKSDIGLTKGCFVSVOGIIT 187
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132  LCFVYPLDFARTRLAADVGSCTEREERGLGDLVITKSDIGLTKGCFVSVOGIIT 190
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      188  RAAYEGVDYTAAGML-DPPKNTIHVSWMIAGTVAVAGVSYDPDVRRRMMQSGRG 246
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      191  RAAYEGVDYTAAGML-DPPKNTIHVSWMIAGTVAVAGVSYDPDVRRRMMQSGRG 249
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      247  ADIMYGVTDCKMRKIFRDEGKAFKFGKAWSNVLKMGCAFVLYVYDELKVI 298
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      250  -DILYKNTLDCAKKTIQNEGSMFEGKALSNVFRGTGALVLAIDEIOKFL 300
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 13

```
115206
hypothetical protein W02D3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T15206
R:Le, T.; Weinstein, L.; Rife, L.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid W02D3.
A:Reference number: 218308
A:Accession: T15206
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <LE>
A:Cross-references: EMBL:AF00341; NID:92088732; PID:92088738; PIDN:AAB54179.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone W02D3
C:Genetic:
A:Gene: CESP:W02D3.6
A:Map position: 1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F:9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
```

```
Query Match      64.4%; Score 993.5; DB 2; Length 300;
Best Local Similarity 64.8%; Pred. No. 2.6e-80;
Matches 195; Conservative 40; Mismatches 59; Indels 7; Gaps 4;
```

```
QY      2  TEOAISFAK--DFLAGGIAAIAISKTAVAPIERVKLLQOVHASKQIADKQKGYDCI 58
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3  TREGDFYRFLVDLASGTAATAVAPIERVKLLQOVDSVSEYTAADKKYKIMDLV 62
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      59  VRIPEQGVLSFWRGNLANVIRYEPFOALNFAFKDKYKQIFLGVDKHTQWRFRFAGNL 118
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      63  ARIPEQGVLSFWRGNLANVIRYEPFOALNFAFKDKYKQIFLGVDKHTQWRFRFAGNL 122
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      119  SGGAGATSLCFVYPLDFARTRLAADVGSCTEREERGLGDLVITKSDIGLTKGCFVS 178
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      123  SGGAGATSLCFVYPLDFARTRLAADVGSCTEREERGLGDLVITKSDIGLTKGCFVS 181
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      179  VSVQGIITRYAAYEGVDYTAAGML-DPPKNTIHVSWMIAGTVAVAGVSYDPDVRRR 237
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182  VSVQGIITRYAAYEGVDYTAAGML-DPPKNTIHVSWMIAGTVAVAGVSYDPDVRRR 241
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      238  MMHMGSRGADIMYGVTDCKMRKIFRDEGKAFKFGKAWSNVLKMGCAFVLYVYDELKVI 297
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      242  MMHMGSRG--DILYKNTLDCVRKIVKNEGITALYKSGLSNVFRATGALVLAIDEIOH 299
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 14

```
A41677
ADP,ATP carrier protein - Chlorella kessleri
C:Species: Chlorella kessleri
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: A41677
R: Hilgath, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A:Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
A:Reference number: A41677; MUID:92084708; PMID:1748677
A:Accession: A41677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <HL>
A:Cross-references: GB:M76669; NID:9516596; PIDN:AAA33027.1; PID:9516597
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F:38-134/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>
```

```
Query Match      63.4%; Score 978; DB 2; Length 339;
Best Local Similarity 66.9%; Pred. No. 7.1e-79;
Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;
```

```
QY      6  ISFAKDFLAGGIAAIAISKTAVAPIERVKLLQOVHASKQIADK--QYKGYDCIARIPK 63
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      39  MAFVKDLAGGTAGATISKTAVAPIERVKLLQOVDSNPMIKSGVPRYGIYVCFVRSS 98
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      64  EGVVLSFWRGNLANVIRYEPFOALNFAFKDKYKQIFLGVDKHTQWRFRFAGNLASGGA 123
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      99  EGVVLSFWRGNLANVIRYEPFOALNFAFKDKYKQIFLGVDKHTQWRFRFAGNLASGGA 157
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      124  GATSLCFVYPLDFARTRLAADVGSCTEREERGLGDLVITKSDIGLTKGCFVSVOG 183
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      158  GATSLCFVYPLDFARTRLAADVGSCTEREERGLGDLVITKSDIGLTKGCFVSVOG 216
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      184  IIVYAAAFGVYDPAKML-DPPKNTIHVSWMIAGTVAVAGVSYDPDVRRRMMQSG 242
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      217  IIVYAAAFGVYDPAKML-DPPKNTIHVSWMIAGTVAVAGVSYDPDVRRRMMQSG 276
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      243  GHKGDIMYGVTDCKMRKIFRDEGKAFKFGKAWSNVLKMGCAFVLYVYDELKVI 298
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      277  ---GGERQYNGTIDCKMRKIFRDEGKAFKFGKAWSNVLKMGCAFVLYVYDELKVI 329
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 15

S51132

```
ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)
N:Alternate names: ADP,ATP transporter
C:Species: Plasmodium falciparum
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C:Accession: S68993; S51132
R: Hall, I.; Jauregui, G.
Eur. J. Biochem. 228, 86-91, 1995
A:Title: Molecular characterization of the ADP/ATP-transporter cDNA from the human ma
A:Reference number: S68993; MUID:95188918; PMID:7883016
A:Accession: S68993
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-301 <HNP>
A:Cross-references: EMBL:X83551; NID:9623334; PIDN:CAA58541.1; PID:9623335
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
```

```
Query Match      61.1%; Score 943; DB 2; Length 301;
Best Local Similarity 61.8%; Pred. No. 7.6e-76;
Matches 183; Conservative 45; Mismatches 62; Indels 6; Gaps 5;
```

7 SFANDFLAGGIAAIAISKTAVAPIERVKLLQOVHASKQIAD--KQYKGYDCIARIPKE 64

```

Db      8  NFAADFLMGISAISKVYVPIERVKMLIQTDISIPEIKSGOVERYSGLINCFRKVSKE 67
Qy      65  OGVLSEFWRGNLANVIRYEPPTQALNPAFKDKYKQIFLGVDKHTQFWRYEPAGNLAGSGANG 124
        68  OGVLSLMRGNVANVIRYEPPTQAFNPAFKDYFNIF-PRYDQNTDPSKFEVCVNLISGATAG 126
Qy      125  ATSLCFVYPLDPAFTRLADAVGKSGTEREFKGLSDCLVKITKSDGIRGLYOGFSYSVOCI 184
        127  AISLLIVYPLDPAFTRLASDICK-GKDRQFTGLFDCLAKIYKQTGILSYSGFVSVTCI 185
Qy      185  IYRAAYFGVYDTAKGML-PDPKNTHIYVSNMIAQTVTAAGVSVSPEDTVRRMMMSG 243
        186  IYRGSYFGIYDSAKALLFTNDKNTINIYLVKMAVAOSVTLIAGLISYPPEDTVRRMMMSG 245
Qy      244  RKG-ADIMYGTVDGWRKIFRDEGGAPEFGKAMSNVLRGMSGAFVLYVDELKVI 298
        246  RKKEEIQYKNTIDCWIKILRNEGFGFEKGAMANYIRGAGALVLYVDELOKLI 301

```

Search completed: August 18, 2003, 16:14:34
 Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 16:02:07 ; Search time 24 Seconds

(without alignments)
583,915 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQALSPKADFLAGGIAA.....LNGMGAPVLYLDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	ADT3_HUMAN*	P12236 homo sapien
2	1512	98.0	298	ADT3_BOVIN*	P32007 bos taurus
3	1463	94.8	298	ADT2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADT2_RAT	O09073 rattus norv
5	1445	93.6	298	ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	ADT1_RAT	O05962 rattus norv
7	1418	91.9	298	ADT1_MOUSE	P48962 mus musculu
8	1417	91.8	297	ADT1_BOVIN	P02732 bos taurus
9	1409	91.3	298	ADT1_HUMAN	P12235 homo sapien
10	1254.5	81.3	299	ADT1_DROME	O26365 drosophila
11	1204	78.0	301	ADT1_ANOGA	O27238 anopheles g
12	978	63.4	339	ADT1_CHLKE	P16632 chlorella k
13	778.5	50.5	307	ADT3_YEAST*	P18238 saccharomyc
14	772	50.0	308	ADT1_CHLRE	P27080 chlamydomon
15	769	49.8	322	ADT1_SCHRO	O09188 schizosacch
16	768	49.8	322	ADT1_GOSHI	O22342 gossypium h
17	766	49.6	313	ADT1_NEUCR	P02723 neurospora
18	762.5	49.4	305	ADT1_KLULA	P49382 kluyveromyc
19	760.5	49.3	318	ADT2_YEAST	P18239 saccharomyc
20	750.5	48.6	385	ADT2_YEAST	P40941 arabidopsis
21	750	48.6	387	ADT1_MAIZE	P04709 zea mays (m
22	748	48.5	386	ADT1_SOLITU	P25083 solanum tub
23	747	48.4	382	ADT1_ORYSA	P16851 oryza sativ
24	744	48.2	387	ADT1_MAIZE	P12857 zea mays (m
25	742.5	48.1	381	ADT1_ARATH	P1187 arabidopsis
26	740	48.0	331	ADT1_WHEAT	O41639 triticum ae
27	739.5	47.9	386	ADT2_SOLITU	P27081 solanum tub
28	737.5	47.8	309	ADT1_YEAST	P04710 saccharomyc
29	727	47.1	331	ADT2_WHEAT	O41630 triticum ae
30	305.5	19.8	565	CMC3_CAEEL	O19529 caenorhabd1
31	302	19.6	588	CMC2_CAEEL	O20799 caenorhabd1
32	300	19.4	330	GDC_BOVIN	O01888 bos taurus
33	299	19.4	307	ODC2_YEAST	O99297 saccharomyc

34	295	19.1	678	1	CMC1_HUMAN	O75746 homo sapien
35	289.5	18.6	322	1	GDC_RAT	P16261 rattus norv
36	287.5	18.6	702	1	CMC1_CAEEL	O21153 caenorhabd1
37	286	18.5	325	1	UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	O922b2 mus musculu
40	282.5	18.3	325	1	YB08_SCHPO	O13805 schizosacch
41	280	18.1	675	1	CMC2_HUMAN	O94350 homo sapien
42	272	17.6	315	1	MFT_HUMAN	O943d1 homo sapien
43	270	17.5	315	1	SA18_HUMAN	O943d1 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	O943x4 mus musculu

ALIGNMENTS

RESULT 1
ADT3_HUMAN STANDARD; PRT; 298 AA.
ID ADT3_HUMAN
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE-2388257; PubMed-2541251;
RX MEDLINE-89236396; PubMed-2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
ADP/ATP translocase".
J. Mol. Biol. 206:261-280(1989).
[2]
SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mel G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
Margolin J.F.;
RL submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE-42388257; PubMed-1247932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Bueltow R.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Dlatcenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Drapelenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Hailton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Ruttenfeld Y.S.N., Krzyzanski M.I., Skalka U., Smalhus D.E.,
Sannech A., Schein J.E., Jones S.D.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-88124845; PubMed-2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

RT level in adult human liver.";
RL PROC. NATL. ACADE. SCI. U.S.A. 85:377-381(1988)
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: J03592; AAA36750.1; -
CC EMBL: AY007135; AAC01998.1; -
CC EMBL: BC007295; AAH07295.1; -
CC EMBL: BC007850; AAH07850.1; -
CC EMBL: BC008737; AAH08737.1; -
CC EMBL: BC008935; AAH08935.1; -
CC EMBL: BC014775; AAH14775.1; -
CC PIR: S03894; S03894.
CC Gene: HSC:10992; SLC25A6.
CC MIM: 303000; -
CC DR MIM: 403005744; C:mitochondrial inner membrane translocase co. .; TMS.
CC DR GO: GO:0005744; F:ATP/ADP antiporter activity; MAS.
CC DR GO: GO:0005471; F:ATP/ADP exchange; TMS.
CC DR InterPro: IPR002067; Mlt_carrier.
CC DR InterPro: IPR002030; Mlt_uncoupling.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carr; 3.
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PRINTS: PR00784; MITOCOUPLING.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.
CC DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC MultiGene family.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 91 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 100 1.
CC FT REPEAT 101 208 2.
CC FT REPEAT 209 298 3.
CC FT REPEAT 105 108 3.
CC FT CONFLICT 242 242 S -> F (IN REF. 3: AAH14775).
CC FT CONFLICT 242 242 S -> F (IN REF. 3: AAH14775).
CC SEQUENCE 298 AA: 32866 MW: 18534 EDPF0549672F CRC64;
Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3; 6e-125;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MTEQATISFANDFLAGGIAAIAISTAVAPIERKYLLOVQVHASKQIAADKQKGYDCTVR 60
DB 1 MTEQATISFANDFLAGGIAAIAISTAVAPIERKYLLOVQVHASKQIAADKQKGYDCTVR 60
DB 61 IPKEQGVLSFWRGKLANIYRFFPTQALNFAFKDKTKQIFLGVDKTHQFWFRFAGNLASG 120
DB 61 IPKEQGVLSFWRGKLANIYRFFPTQALNFAFKDKTKQIFLGVDKTHQFWFRFAGNLASG 120
DB 61 IPKEQGVLSFWRGKLANIYRFFPTQALNFAFKDKTKQIFLGVDKTHQFWFRFAGNLASG 120
DB 121 GAAGATSLCFYVPLDFATRIADVGSKTEREERFGLGDCLVKTKSDGIRGLYQGFSSVS 180
DB 121 GAAGATSLCFYVPLDFATRIADVGSKTEREERFGLGDCLVKTKSDGIRGLYQGFSSVS 180
DB 121 GAAGATSLCFYVPLDFATRIADVGSKTEREERFGLGDCLVKTKSDGIRGLYQGFSSVS 180
DB 181 VGGIITTYRAAYGVVDYDKGMLPDKKTHIVVSWMLAQTVAIVAGVVSYPEDTVRRMM 240
DB 181 VGGIITTYRAAYGVVDYDKGMLPDKKTHIVVSWMLAQTVAIVAGVVSYPEDTVRRMM 240

QY 241 QSGRKADIMTYGTVDCKRIFRDEGKAFKFGAMSNVLRMGCAFVLVYLDLKKVY 298
DB 241 QSGRKADIMTYGTVDCKRIFRDEGKAFKFGAMSNVLRMGCAFVLVYLDLKKVY 298
RESULT 2
ADP3_BOVIN STANDARD; PRT; 298 AA.
ID ADP3_BOVIN
DR P32007; 1993 (Rel. 26, Created)
DR 01-001-1993 (Rel. 26, Last sequence update)
DR 01-001-1993 (Rel. 40, Last annotation update)
DR 16-001-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, isoform 12 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP MEDLINE=89229093; PubMed=2540808;
RX Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RA "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RT Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC
CC EMBL: M24103; AA30769.1; -
CC PIR: B43646; B43646.
CC DR InterPro: IPR002067; Mlt_carrier.
CC DR InterPro: IPR002030; Mlt_uncoupling.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carr; 3.
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PRINTS: PR00784; MITOCOUPLING.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.
CC DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC MultiGene family.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 91 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 111 1.
CC FT REPEAT 112 208 2.
CC FT REPEAT 209 298 3.
CC SEQUENCE 298 AA: 1C34E7DFE6DE4061 CRC64;
Query Match 98.0%; Score 1512; DB 1; Length 298;
Best Local Similarity 97.7%; Pred. No. 1; 9e-125;
Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
DB 1 MTEQATISFANDFLAGGIAAIAISTAVAPIERKYLLOVQVHASKQIAADKQKGYDCTVR 60
DB 1 MTEQATISFANDFLAGGIAAIAISTAVAPIERKYLLOVQVHASKQIAADKQKGYDCTVR 60

```

QY 61 IPKEGVLSPWNGNLNANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLAGS 120
CC |||
CC 61 IPKEGVLSPWNGNLNANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLAGS 120
Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVYKITSDDIRGLYQGFVS 180
QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVYKITSDDIRGLYQGFVS 180
Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVYKITSDDIRGLYQGFVS 180
QY 181 VOGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRRMM 240
CC |||
CC 181 VOGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRRMM 240
Db 181 VOGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRRMM 240
QY 241 QSGRKADIMYGTGVCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELKRYI 298
CC |||
CC 241 QSGRKADIMYGTGVCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELKRYI 298
Db 241 QSGRKADIMYGTGVCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELKRYI 298

RESULT 3
ADP2_HUMAN STANDARD: PRT; 298 AA.
ID ADP2_HUMAN. P05141; O43350;
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, last sequence update)
DT 01-OCT-1994 (Rel. 30, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
DE SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE-90375457; PubMed-2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence.
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-87166056; PubMed-3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated".
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagara J.A.,
RA Mazzerella R.A., Schlessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozerzky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE-88124845; PubMed-2829183;
RA Houldsworth J., Attardi G.;
RT Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57424; AAA51737.1; -
DR EMBL; J02683; AAA35579.1; -
DR EMBL; I78810; AAB39266.1; -
DR EMBL; AC004000; AAB96547.1; -
DR EMBL; J03591; AAA36749.1; -
DR PIR; A29132; A29132.
DR Genew; HGNC; 10991; SLC25A5.
DR MIM; 300150; -
DR GO; GO:0005887; C: Integral to plasma membrane; TAS.
DR GO; GO:0015207; F: adenine transporter activity; TAS.
DR GO; GO:0006832; P: small molecule transport; TAS.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUOCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; P973C3ABD92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;
Best Local Similarity 92.9%; Pred. No. 3, 8e-121;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDPLAGIAAIAISTAVAPIERVALLQVOHASKQIAADKQYKIVDCYR 60
||: |||
Db 1 MTEQATSPAKDPLAGIAAIAISTAVAPIERVALLQVOHASKQIAADKQYKIVDCYR 60
QY 61 IPKEGVLSPWNGNLNANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLAGS 120
|||
Db 61 IPKEGVLSPWNGNLNANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVYKITSDDIRGLYQGFVS 180
|||
Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVYKITSDDIRGLYQGFVS 180
QY 181 VOGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRRMM 240
|||
Db 181 VOGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRRMM 240
QY 241 QSGRKADIMYGTGVCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELKRYI 298
|||
Db 241 QSGRKADIMYGTGVCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELKRYI 298

RESULT 4
ADP2_RAT STANDARD: PRT; 298 AA.
ID ADP2_RAT. P09073;
AC P09073;
DT 01-FEB-1995 (Rel. 31, Created)

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01-FEB-1995 (Rel. 31, last sequence update)
 16-OCT-2001 (Rel. 40, last annotation update)
 ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 (Adenine nucleotide translocator 2) (ANT 2).
 DE SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamada M., Yamazaki N., Terada H.;
 RT Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.;
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D12771; BAA0238.1; -;
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mltc_car; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;
 Query Match 94.0%; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.9%; Pred No 4.3e-120;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQATSPKADPLAGLAAISTKAVAPIERKLLQVQVHASKQIADKQYKIVCYR 60
 DB 1 MTDAAVSFKDFKPLAGVAAVIASTKAVAPIERKLLQVQVHASKQIADKQYKIVCYR 60
 QY 61 IPREGVLSFWKGNLANVIRYFTQALNFAFDKTKQIFLGVDKHTQFWRFRAGNIASG 120
 DB 61 IPREGVLSFWKGNLANVIRYFTQALNFAFDKTKQIFLGVDKHTQFWRFRAGNIASG 120
 QY 121 GAAGATSLCFYVPLDFAFTRIAADVGSKTEERFGIDCLVTKTSKDGIRNGLYOGFSYS 180
 DB 121 GAAGATSLCFYVPLDFAFTRIAADVGSKTEERFGIDCLVTKTSKDGIRNGLYOGFSYS 180
 QY 181 VGGIITRYAAAFGVYDRAKGLPDKNTHIVVSMIAQVTVAVAGVVSYPEDIVRRMM 240

181 VGGIITRYAAAFGVYDRAKGLPDKNTHIVVSMIAQVTVAVAGVVSYPEDIVRRMM 240
 241 OSGRKADIMTYGTDCWRKTFRDEGKAFKAGNSVLRGSGAFVLYLDELTK 296
 241 OSGRKADIMTYGTDCWRKTFRDEGKAFKAGNSVLRGSGAFVLYLDELTK 296
 RESULT 5
 ADT2_MOUSE STANDARD; PRT: 298 AA.
 AC P51881; Q61311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RT homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RL (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995); University of Cambridge, U.K.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Costet P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: U27316; AAC5288.1; -;
 DR EMBL: U10404; AAA1909.1; -;
 DR EMBL: X70847; CAA50196.1; -;
 DR EMBL: AF240003; AAF64471.1; -;
 DR MGD: MGI:1353496; SLC25A5.
 DR InterPro: IPR002067; Mlt_carrier.

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DR InterPro: IPR002030; Mit. uncoupling.
DR InterPro: IPR001993; Mitoch. carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 93.6%; Score 1445; DB 1; Length 298;
Best Local Similarity 91.6%; Pred. No. 1,4e-119;
Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIADKQKIVDCIVR 60
DB 1 MDAAVSFADDFLAGGAAISTAVAPIERVKLLQVQHASKOITADKQKIIDCVR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNIASG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNIASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSDDIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSDDIRGLYOGFSVS 180
QY 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFPDVRRRMM 240
DB 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFPDVRRRMM 240
QY 241 QSGRKGADIMYTGTVDCWKRIFDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296
DB 241 QSGRKGADIMYTGTVDCWKRIFDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296

RESULT 6
ADTL_RAT STANDARD; PRT; 298 AA.
ID ADTL_RAT STANDARD; PRT; 298 AA.
AC 005962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Blochum. Blochum. Acta 1152:192-196(1993)
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.

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CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
DR EMBL: X61667; CAA3842.1; -.
DR EMBL: D12770; BA02237.1; -.
DR FTR: 160173; 160173.
DR InterPro: IPR002067; Mit. carrier.
DR InterPro: IPR002030; Mit. uncoupling.
DR InterPro: IPR001993; Mitoch. carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1e-117;
Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIADKQKIVDCIVR 60
DB 1 MDAQALSLDFLAGGIAAIVSTAVAPIERVKLLQVQHASKOISERKQKIIDCVR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNIASG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNIASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSDDIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSDDIRGLYOGFSVS 180
QY 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFPDVRRRMM 240
DB 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFPDVRRRMM 240
QY 241 QSGRKGADIMYTGTVDCWKRIFDEGKAFKFGAMSVNLGMCAPVLYLYDELK 298
DB 241 QSGRKGADIMYTGTVDCWKRIFDEGKAFKFGAMSVNLGMCAPVLYLYDELK 298

RESULT 7
ADTL_MOUSE STANDARD; PRT; 298 AA.
ID ADTL_MOUSE STANDARD; PRT; 298 AA.
AC P48962; Q62164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MNC1).
GN SLC25A4 OR ANT1 OR MNC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

```

RN [1] SEQUENCE FROM N.A.
 RC STRAIN-6/6; TISSUE-Brain;
 RX MEDLINE-97059403; PubMed-8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-2388257; PubMed-12477932;
 RA Krauss R.D., Collins F.S., Wagner L., Shenman G.M., Schuler G.D.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Marusik K., Farmer A., Rubin G.M., Hong L.,
 RA Datchenko U., Maust K., Bonaldo M.P., Casavant T.F., Scheetz T.E.,
 RA Branstetter M., Olson J.B., Roshylyk S., Carninci P., Prange C.,
 RA Kohn S.S., Lodigiano N.A., Peters G.J., Abramson R.D., Millar S.J.,
 RA Bork S.A., McSwan P.J., McKernan K.J., Malek J.A., Cunniff P.H.,
 RA Villalón D., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Whiting J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maita M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [1] FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC [1] SUBUNIT: Homodimer.
 CC [1] SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC [1] DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC [1] SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: UZ7315; AAC52837.1; -;
 DR EMBL: X74510; CAA52616.1; -;
 DR EMBL: AF240002; AAF64470.1; -;
 DR EMBL: BC003791; AAH03791.1; -;
 DR EMBL: BC026925; AAH26925.1; -;
 DR PIR: S37210; S37210.
 DR MGI: MGI:1353495; Slc25a4.
 DR InterPro: IPR002067; Mtl_carrier.
 DR InterPro: IPR002030; Mtl_uncarrier.
 DR InterPro: IPR001993; Mtlc_carrier.
 DR Pfam: PF00153; mtlc_carrier_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 3 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 136 136 F -> L (IN REF. 1).
 FT CONFLICT 136 136
 FT SEQUENCE 298 AA; 32904 MW; 3A849FEB0981462 CRC64;
 SQ
 Query Match 91.9%; Score 1418; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 3,4e-117;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
 OY 1 MTEQAISFANDFLAGGIAAIAISKTAVAPIERVKLLQVOHASKQIAADKQXKGIYDCTR 60
 DB 1 MGDAISFLKDFLAGGIAAIAVSKTAVAPIERVKLLQVOHASKQIAADKQXKGIYDCTR 60
 OY 61 IPKRGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 120
 DB 61 IPKRGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 120
 OY 121 GAAGATSLCFVYPLDPAFRTPLAADVGKSGTEREPRGLDCLVYITKSDIRGLYGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTPLAADVGKSGTEREPRGLDCLVYITKSDIRGLYGFVS 180
 OY 121 GAAGATSLCFVYPLDPAFRTPLAADVGKSGTEREPRGLDCLVYITKSDIRGLYGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTPLAADVGKSGTEREPRGLDCLVYITKSDIRGLYGFVS 180
 OY 161 VGGITIRAVFVYPTAKGMLPDPKNTIYVSMINQOTYAVAGVSPFTYRRMM 240
 DB 161 VGGITIRAVFVYPTAKGMLPDPKNTIYVSMINQOTYAVAGVSPFTYRRMM 240
 OY 241 OSGRKGDIVTYTCWCKRIFRDEGKAFKAGSNVNLGMCAGVLYLYELKKVI 298
 DB 241 OSGRKGDIVTYTCWCKRIFRDEGKAFKAGSNVNLGMCAGVLYLYELKKVI 298
 DB 241 OSGRKGDIVTYTCWCKRIFRDEGKAFKAGSNVNLGMCAGVLYLYELKKVI 298
 RESULT 8
 ADT1_BOVIN STANDARD; PRT: 297 AA.
 ID ADT1_BOVIN
 AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart isoform 71 (ADP/ATP translocase 1)
 DE (Adenine nucleotide translocator 1) (ANT 1).
 GN SLc25A4 OR ANT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RX MEDLINE-89229093; PubMed-2540808;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
 RT differences in various tissues.";
 RL Biochemistry 28:866-873(1989).
 RN [2]
 RP SEQUENCE.
 RA MEDLINE-82188267; PubMed-7076130;
 RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
 RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
 RT mitochondria.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
 RN [3]
 RP SEQUENCE OF 207-297 FROM N.A.
 RX MEDLINE-86295775; PubMed-3017341;
 RA Rasmussen U.B., Wohlrab R.;
 RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

RT an unusually short 3'-noncoding sequence";
 CC Blochem. Biophys. Res. Commun. 138:850-857(1986).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL: M13783; AAA30363.1; -;
 CC EMBL: M24102; AAA30768.1; -;
 CC PIR: A43646; XMO.
 CC InterPro: IPR002067; Mt_carrier.
 CC InterPro: IPR002030; Mt_uncoupling.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr. 3
 CC PRINTS: PR00926; MITOCARRIER.
 CC PRINTS: PR00784; MTUNCOUPLING.
 CC PROSITE: PS00215; MITOCH_CARRIER; 3.
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Methylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 BLOCKED.
 FT MOD_RES 51 51 METHYLATION (POTENTIAL).
 FT TRANSMEM 11 28 1 (POTENTIAL).
 FT TRANSMEM 72 90 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 175 194 4 (POTENTIAL).
 FT TRANSMEM 213 230 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 207 2.
 FT REPEAT 208 297 3.
 SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;
 Query Match 91.8%; Score 1417; DB 1; Length 297;
 Best Local Similarity 89.2%; Pred. No. 4.1e-117;
 Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
 QY 2 TQGAISFADFLAGGTAIAISKTAVAPIERVKLLQVQHASKQIADKQKGIIVDCIVRI 61
 DB 1 SDQALSFELDFLAGVAAISKTAVAPIERVKLLQVQHASKQISAEKQKGIIVDCIVRI 60
 QY 62 PRQGVLSFWRGNIANVIRFPTQALNFAFKDKYKQIFGQVVDKHFQFMFYFAGNLASGG 121
 DB 61 PRQGVLSFWRGNIANVIRFPTQALNFAFKDKYKQIFGQVVDKHFQFMFYFAGNLASGG 120
 QY 122 AAGASLSCVYPLDEAFRIADLVGSKGTEREFGIGDCLVTKTSKDGKIGLQYGSVSY 181
 DB 121 AAGASLSCVYPLDEAFRIADLVGSKGTEREFGIGDCLVTKTSKDGKIGLQYGSVSY 180
 QY 182 OGIIIRAAVFGYVDAAKGMILPDKRTHIVSWMIAQYTAAGVSYSPEDTVRRRMMQ 241
 DB 181 OGIIIRAAVFGYVDAAKGMILPDKRTHIVSWMIAQYTAAGVSYSPEDTVRRRMMQ 240
 QY 242 SGRKGAIDMYTGTGVDCKRIIFRDEGKRAFEFGKAMSVNLKMGGAFLVLYDELKRYI 298
 DB 241 SGRKGAIDMYTGTGVDCKRIIFRDEGKRAFEFGKAMSVNLKMGGAFLVLYDELKRYI 297
 RESULT 9
 ID ADT1_HUMAN
 AC P12235; STANDARD; PRT; 298 AA.

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons,
 RT is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13998-14004(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041149; PubMed=2823266;
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,
 RT and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houlsworth J., Atcari G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PRO-114 AND MET-289.
 RX MEDLINE=20385067; PubMed=10926541;
 RA Kaukonen J., Jusellius J.K., Tiranli V., Kyttala A., Zeviani M.,
 RA Comi G.P., Keranen J., Peltonen L., Somatalen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC	MITOCHONDRIAL INNER MEMBRANE.
CC	-1- SUBUNIT: Homodimer.
CC	-1- SUPRACELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC	-1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC	EMBL; J02966; AAA61223.1; -
DR	EMBL; J03593; AAA36751.1; -
DR	EMBL; J04982; AAA51736.1; -
DR	EMBL; BC008664; AAH08664.1; -
DR	PIR; A44778; A44778.
DR	Genew; HGNC:10990; SLC25A4.
DR	MIM; 103220; -
DR	MIM; 157640; -
DR	GO; GO:000587; C:Integral to Plasma membrane; TAS.
DR	GO; GO:0005739; C:mitchondrion; TAS.
DR	GO; GO:0015207; F:adenine transporter activity; TAS.
DR	GO; GO:0006091; F:energy pathway; TAS.
DR	GO; GO:0000002; P:mitochondrial genome maintenance; TAS.
DR	GO; GO:0006833; P:small molecule transport; TAS.
DR	InterPro; IPR002067; MLC_carrier.
DR	InterPro; IPR002030; MLC_uncoupling.
DR	InterPro; IPR001993; Mitoch_carrier.
DR	Pfam; PF00153; mito_carr; 3
DR	PRINTS; PR00926; MITOCARRIER.
DR	PRINTS; PR00784; MTUNCOUPLING.
KW	PROSITE; PS00215; MITOCH_CARRIER; 3.
RK	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
RY	Multigene family; Disease mutation
FT	TRANSMEM 73 29 1 (POTENTIAL).
FT	TRANSMEM 91 2 1 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 214 231 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 1 110 1.
FT	REPEAT 111 208 2.
FT	REPEAT 209 298 3.
FT	VARIANT 114 114 A-> P (IN PRO).
FT	VARIANT 289 289 V-> M (IN PRO).
FT	CONFLICT 16 16 G-> A (IN REF. 3).
FT	CONFLICT 147 149 CGA-> RR (IN REF. 3).
FT	CONFLICT 227 227 KCA-> L (IN REF. 3).
SO	SEQUENCE 298 AA; 33064 MW; 59F0DPAECA4EFCRB CRC64;
Oy	Best Local Similarity 91.3%; Score 1409; DB 1; Length 298;
Db	Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
Oy	1 MTEDAISPAKDQFLAGGIAAAIKTNVAPIERVKLLQOVHASKQTADKDTKIIVDCYR 60
Db	1 MEDHAMSLWDLPDLGGVAAAASKTAIVAPIERVKLLQOVHASKQTASAKDKIIDCYVR 60
Oy	61 IPKDEGVLSFWRCNLANVTIRPTQALNFAPFKDYKQIFLGVDVKHRNQFWRYEAGNLASG 120
Db	61 IPKDEGVLSFWRCNLANVTIRPTQALNFAPFKDYKQKYLETGVDGRHNHQFWRYEAGNLASG 120

OY		123	GAGATGTCSCFEYPPLDEFAKRTBLADYGKSQTEREGRGLDCLVITRSDGIRLXYGFSVS	180
Dd		121	GAAATGTCSCFEYPLDPFARFTBLADYGKGAORERFHGIIDCIIKIFMSDLRGTYGFNWS	180
OY		181	VGGIITTAATAAFEGYVDPAKGMLPDKRNTHIVSMNTAOYTANAVGVSVPEPTVRBRBM	240
Dd		181	VGGIITTAATAAFEGYVDPAKGMLPDKRNTHIVSMNTAOSTANAGLVSPEDPTVRBRBM	240
OY		241	OSGRGAGDIAMTGYCNVCCHRRTRDRDGCAFRCFGAWNVLLMGACAVLVLYDELKRYI	298
Dd		241	OSGRGAGADIIMTGTVIDCMKRINADEGAKAFRCGAWNVLLMGCAFEVLVLDELIKRYI	298
RESULT 10				
ADT_DROME				
ID	ADT_DROME	STANDARD;	PRT; 299 AA.	
AC	Q26365; P1614; Q26254; Q95S30; g9vz70;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT) (Stress sensitive B protein).			
GN	SEB OR A/A-T OR CG16944.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
OX	NBI_TaxId=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92389367; PubMed=1387687;			
RA	Louvi A., Tselicou S.G.;			
RT	A cDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases."			
RL	J. Mol. Evol. 35:44-50(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94350065; PubMed=7520869;			
RA	Hutter P., Karch F.;			
RT	"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila."			
RL	Experientia 50:749-762(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Berkeley;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanalidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Abghyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S., Borokov K.C., Botchan M.R., Bouck J., Brockstein P., Brodtier P., Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Crowley S., Dahlke C., Daveport L.B., Davies P., de Paulis B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Garay N.S., Gelbart W.M., Fleischmann W., Foster C., Gabriellian A.E., Gary N.S., Gebart W.S., Glasser K., Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwu C., Jalali M., Kalish J., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,			

FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9FDA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;
 Best Local Similarity 77.7%; Pred. No. 2, 1e-98;
 Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

OY 1 MTRKADPFGAFKDFLAGISNAVSKTAVAPIERVKLLQVQASQIADVKQYGYDTC 58
 DB 1 MTRKADPFGAFKDFLAGISNAVSKTAVAPIERVKLLQVQASQIADVKQYGYDTC 60
 OY 59 VRIPEKOGVLSFMRGNLANVIRPEPTQALNFAFKDKYKOIFLGGVDKHTQFMRPFAAGNTA 118
 DB 61 VRIPEKOGVLSFMRGNLANVIRPEPTQALNFAFKDKYKOIFLGGVDKHTQFMRPFAAGNTA 120
 OY 119 SGGAAGATSLCEVYPLDFAFRTLAADVKGSGTEREFGDCLVTKTSKDSIRGLYOGFS 178
 DB 121 SGGAAGATSLCEVYPLDFAFRTLAADVKGSGTEREFGDCLVTKTSKDSIRGLYOGFS 180
 OY 179 VSVGGIIRAAVFGVYDFAKGMPLDPKNTIIVSMIQTAVAGVSYPEPTVRRRM 238
 DB 181 VSVGGIIRAAVFGVYDFAKGMPLDPKNTIIVSMIQTAVAGVSYPEPTVRRRM 240
 OY 239 MMSGGRGADIMYTGVCNMRKIFRDGKAFKAGMSNVLRGKGAFVLYDELKTV 298
 DB 241 MMSGGRGADIMYTGVCNMRKIFRDGKAFKAGMSNVLRGKGAFVLYDELKTV 300

RESULT 12
 ADT_CHLKE STANDARD; PRT; 339 AA.

AC P31692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 OS Chlorella kessleri.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorellia.
 NCBI_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-92084708; PubMed-1748677;
 RA Hilgarch C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 CC EMBL: M76669; AAA33027.1; -
 CC PIR: A41677; A41677.
 CC Interpro: IPR002067; Mit_carrier.
 CC Interpro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr; 3.
 CC PRINTS: PRO0926; MITOCH_CARRIER.
 CC PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A3B3942 CRC64;

Query Match 63.4%; Score 978; DB 1; Length 339;
 Best Local Similarity 66.9%; Pred. No. 1, 6e-78;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

OY 6 ISFADPFLAGIAAISKTAAPAPIERVKLLQVQASQIADVK-QYKGYDTCYRIK 63
 DB 39 MAFVMDLAGTAGAISKTAAPAPIERVKLLQVQASQIADVK-QYKGYDTCYRIK 98
 OY 64 EGVLSFMRGNLANVIRPEPTQALNFAFKDKYKOIFLGGVDKHTQFMRPFAAGNTA 123
 DB 99 EGVLSFMRGNLANVIRPEPTQALNFAFKDKYKOIFLGGVDKHTQFMRPFAAGNTA 157
 OY 124 GATSLCEVYPLDFAFRTLAADVKGSGTEREFGDCLVTKTSKDSIRGLYOGFSYVSG 183
 DB 158 GATSLCEVYPLDFAFRTLAADVKGSGTEREFGDCLVTKTSKDSIRGLYOGFSYVSG 216
 OY 184 IIVYRAVFGVYDFAKGMPLDPKNTIIVSMIQTAVAGVSYPEPTVRRRM 242
 DB 217 IIVYRAVFGVYDFAKGMPLDPKNTIIVSMIQTAVAGVSYPEPTVRRRM 276
 OY 243 GRRGADIMYTGVCNMRKIFRDGKAFKAGMSNVLRGKGAFVLYDELKTV 298
 DB 277 ---GGERQYNGTIDCMRKVAQCEGMAFFKAGMSNVLRGKGAFVLYDELKTV 329

RESULT 13
 ADT3_YEAST STANDARD; PRT; 307 AA.

AC P18238;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP, ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).
 GN AAC3 OR YBR085W OR YBR0753.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-90324269; PubMed-2165073;
 RA Kolarov J., Kolarova N., Nelson N.;
 RT "A third ADP/ATP translocator gene in yeast.";
 RL J. Biol. Chem. 265:12711-12716(1990).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN-S288C;
 CC Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
 CC Vissers S.;
 CC Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC SEQUENCE OF 38-307 FROM N.A.
 CC STRAIN-S288C;
 CC Feldmann H., Manhaupt G., Schwarzlose C., Vetter I.;
 CC Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----

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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:08:37 ; Search time 97 Seconds
(without alignments)
792.780 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEQAIISFAKDFLAGGIAAA.....LRGCGAFVLYLDELKVI 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

- 1: SP_archaea:*
- 2: SP_bacteria:*
- 3: SP_fungi:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_virus:*
- 16: SP_bacteriap:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1474	95.5	298	13	OBAYM3
2	1451	94.0	298	6	OB8QHS
3	1446	93.7	298	13	OB8TH0
4	1422	92.2	298	6	O46373
5	1421	92.1	298	13	O919M9
6	1414	91.6	298	11	OB8V19
7	1409	91.3	298	13	O9PRH1
8	1406	91.1	298	13	O9PRH2
9	1402	90.9	298	13	O9YIC4
10	1300	84.3	299	5	O95VX4
11	1259	81.6	317	13	O91336
12	1254.5	80.1	312	5	O8IRAO
13	1235.5	80.1	300	5	O9NHW5
14	1187.5	77.0	288	5	O44093
15	1183.5	76.7	288	5	O44094
16	1176.5	76.2	304	5	O25129

17	1159	75.1	254	11	OB8K05	OB8K05 mus musculus
18	1137.5	73.7	307	5	O62526	O62526 drosophila
19	1119	72.5	315	4	O9HOC2	O9HOC2 homo sapien
20	1041	67.5	313	5	O21103	O21103 caenorhabd1
21	1039	67.3	313	5	P91410	P91410 caenorhabd1
22	1038	67.3	300	5	O45865	O45865 caenorhabd1
23	1036.5	67.2	310	10	O8H727	O8H727 phytothor
24	996	64.5	309	5	O97470	O97470 dictyostell
25	993.5	64.4	300	5	O01813	O01813 caenorhabd1
26	993	64.4	300	5	O17407	O17407 caenorhabd1
27	973.5	63.1	318	5	O9BJ36	O9BJ36 toxoplasma
28	947	61.4	301	5	O8IU34	O8IU34 plasmodium
29	946.5	61.3	307	8	O9XM22	O9XM22 ascaris sun
30	944	61.2	301	5	O25692	O25692 plasmodium
31	943	61.1	301	5	OB8WY4	OB8WY4 euploetes sp
32	943	60.7	305	5	O26006	O26006 plasmodium
33	936	60.7	305	5	OB8WY7	OB8WY7 nyctotherus
34	932	60.4	308	5	OB8WY8	OB8WY8 nyctotherus
35	924	59.9	306	5	OB8WY5	OB8WY5 nyctotherus
36	924	59.9	308	5	OB8WY6	OB8WY6 nyctotherus
37	827	53.6	170	6	O9X569	O9X569 sus scrofa
38	778.5	50.5	305	3	O9P8M1	O9P8M1 yarrowia 11
39	767.5	49.7	302	3	O8J0M2	O8J0M2 yarrowia 11
40	764	49.5	326	5	P91270	P91270 caenorhabd1
41	760	49.3	307	5	O76286	O76286 trypanosoma
42	759	49.2	303	3	O74260	O74260 candida par
43	756.5	49.0	306	5	O18683	O18683 caenorhabd1
44	753	48.8	307	5	O26697	O26697 trypanosoma
45	749	48.5	315	3	O8J0U1	O8J0U1 gaemannomy

ALIGNMENTS

RESULT 1

ID	OBAYM3	PRELIMINARY	PRT	298 AA.
AC	OBAYM3			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	ATP/ADP antiporter.			
GN	AVANT.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;			
RT	"Cold-induced mitochondrial uncoupling and expression of chicken UCP			
RT	and ANT mRNA in chicken skeletal muscle.";			
RL	FEBS Lett. 0:0-0(2002).			
DR	EMBL; AB086866; BAC15533.1; -			
SQ	SEQUENCE 298 AA; 32847 MW; 1174CSECA400A10D CRC64;			

Query Match	95.5%	Score 1474;	DB 13;	Length 298;
Best Local Similarity	93.0%	Pred. No. 2.5e-125;		
Matches 277;	Conservative 14;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1	MTEQAIISFAKDFLAGGIAAAISKTAAPIERVVLLIQVHASKQIADKQKGVDCIYR	60	
DB	1	MDQAIISFLKDFLAGGIAAAISKTAAPIERVVLLIQVHASKQIADKQKGVDCIYR	60	
QY	61	IREQGVLSFWKGNLANVIRFPTQALNFAFKDKYQIFLGVDKTKTQWRFPAGWLASG	120	
DB	61	IREQGVLSFWKGNLANVIRFPTQALNFAFKDKYQIFLGVDKTKTQWRFPAGWLASG	120	
QY	121	GAAGATSLCFVYPLDFARTRIADVGKSGEREFRGLGCLVITKSDGIRGLYOGFYS	180	
DB	121	GAAGATSLCFVYPLDFARTRIADVGKSGEREFRGLGCLVITKSDGIRGLYOGFYS	180	

QY 181 VGGIIIRAAVFGVDTAKGMLPDKRNTHIVSMIAQVTVAVGVSTPDTYRRMM 240
|||||
DB 181 VGGIIIRAAVFGVDTAKGMLPDKRNTHIVSMIAQVTVAVGVSTPDTYRRMM 240
241 QSGRRGADIMYTGTVDCKMKIRFDEGKAFFKAGMSVNLKMGAFVLYLDELKRV 298
|||||
DB 241 QSGRRGADIMYTGTVDCKMKIRFDEGKAFFKAGMSVNLKMGAFVLYLDELKRV 298

RESULT 2

08SOH5 PRELIMINARY; PRT; 298 AA.

DB 01-JUN-2002 (TREMBLREL. 21, Created)
DB 01-JUN-2002 (TREMBLREL. 21, Last sequence update)
DB 01-MAR-2003 (TREMBLREL. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine); Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Cephalodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shiohara Y., Tanida K., Terada H.;
RT Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms.
RL Mitochondrion 1:371-379 (2002).
DR EMBL: AB065433; BAB84673.1;
DR InterPro: IPR001993; Mitochondrion.
DR Pfam: PF00153; mito_carrier.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;
Best Local Similarity 92.2%; Pred. No. 3e-123;
Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDFLAGGIAAISTKTAFAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
|||
DB 1 MTEQATSPAKDFLAGGIAAISTKTAFAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
61 IPKRGVLSFWRGNLANVIRYFPPOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAG 120
|||
DB 61 IPKRGVLSFWRGNLANVIRYFPPOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAG 120
121 GAAGATSLCFYVPLDPAKTRLAADVSGTEREFGIDCLVITKSDGIRGLYOGFVS 180
|||||
DB 121 GAAGATSLCFYVPLDPAKTRLAADVSGTEREFGIDCLVITKSDGIRGLYOGFVS 180
181 VGGIIIRAAVFGVDTAKGMLPDKRNTHIVSMIAQVTVAVGVSTPDTYRRMM 240
|||||
DB 181 VGGIIIRAAVFGVDTAKGMLPDKRNTHIVSMIAQVTVAVGVSTPDTYRRMM 240
241 QSGRRGADIMYTGTVDCKMKIRFDEGKAFFKAGMSVNLKMGAFVLYLDELKRV 298
|||||
DB 241 QSGRRGADIMYTGTVDCKMKIRFDEGKAFFKAGMSVNLKMGAFVLYLDELKRV 298

RESULT 3

08JH10 PRELIMINARY; PRT; 298 AA.

DB 01-OCT-2002 (TREMBLREL. 22, Created)
DB 01-OCT-2002 (TREMBLREL. 22, Last sequence update)
DB 01-MAR-2003 (TREMBLREL. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
OS Brachydanio rerio (Zebrafish); Danio rerio.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

OK NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:2205902; PubMed:12006978;
RA Golling G., Amstutz A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Atz K., Farrington S., Lin S.-Y., Nissen R.M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development."
RL Nat. Genet. 31:135-140 (2002).
DR EMBL: AF506216; AAM34650.1;
DR InterPro: IPR001993; Mitochondrion.
DR InterPro: IPR002067; Mitochondrion.
DR InterPro: IPR002030; Mitochondrion.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCH_CARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;

Query Match 93.7%; Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 8.5e-123;
Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDFLAGGIAAISTKTAFAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
|||
DB 1 MTEQATSPAKDFLAGGIAAISTKTAFAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
61 IPKRGVLSFWRGNLANVIRYFPPOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAG 120
|||||
DB 61 IPKRGVLSFWRGNLANVIRYFPPOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAG 120
121 GAAGATSLCFYVPLDPAKTRLAADVSGTEREFGIDCLVITKSDGIRGLYOGFVS 180
|||||
DB 121 GAAGATSLCFYVPLDPAKTRLAADVSGTEREFGIDCLVITKSDGIRGLYOGFVS 180
181 VGGIIIRAAVFGVDTAKGMLPDKRNTHIVSMIAQVTVAVGVSTPDTYRRMM 240
|||||
DB 181 VGGIIIRAAVFGVDTAKGMLPDKRNTHIVSMIAQVTVAVGVSTPDTYRRMM 240
241 QSGRRGADIMYTGTVDCKMKIRFDEGKAFFKAGMSVNLKMGAFVLYLDELKRV 298
|||||
DB 241 QSGRRGADIMYTGTVDCKMKIRFDEGKAFFKAGMSVNLKMGAFVLYLDELKRV 298

RESULT 4

046373 PRELIMINARY; PRT; 298 AA.

AC 046373;
DB 01-JUN-1998 (TREMBLREL. 06, Created)
DB 01-JUN-1998 (TREMBLREL. 06, Last sequence update)
DB 01-MAR-2003 (TREMBLREL. 23, Last annotation update)
DE ADP/ATP translocase.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Skeletal muscle;
RA Yamaguchi N., Kasai M.;
RT Identification of a 30kDa calsequestrin-binding protein, which
RT regulates calcium release from sarcoplasmic reticulum of rabbit
RT skeletal muscle.
RL J. Biochem. 335:541-547 (1998).
CC EMBL: AB009386; BAA3777.1;
DR InterPro: IPR001993; Mitochondrion.
DR InterPro: IPR002067; Mitochondrion.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCH_CARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.

DR PROSITE: PS00215; MITOCH_CARRIER: 3.
SQ Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;
Best Local Similarity 88.9%; Pred. No. 1.3e-120;
Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
DB 1 MSQALSLFKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
QY 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
QY 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298

RESULT 5
Q919M9 PRELIMINARY; PRT; 298 AA.

AC 0919M9; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355.
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -; SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF231347; AAF63471.1; -
DR Interpro: IPR001993; Mitoch_carrier.
DR Interpro: IPR002067; Mit_carrier.
DR Interpro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carrier_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;
Best Local Similarity 90.3%; Pred. No. 1.6e-120;
Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
QY 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
QY 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298

Query Match 91.6%; Score 1414; DB 11; Length 298;
Best Local Similarity 88.6%; Pred. No. 6.8e-120;
Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
QY 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
QY 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298

RESULT 6
Q98BV19 PRELIMINARY; PRT; 298 AA.

AC 098BV19; 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=2354683; PubMed=12466851;
RA The FANTOM Consortium.
RA "The Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK078077; BAC37117.1; -
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 91.6%; Score 1414; DB 11; Length 298;
Best Local Similarity 88.6%; Pred. No. 6.8e-120;
Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKIVDCIVR 60
QY 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEGVLSPWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDGLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSMTIAQVTVAVAGVSYDFDVRRRMM 240
QY 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVDCMKRIFFDEGKAFKFGKAMSVNLGKMGAFVLYLDELKRYI 298

OX NCBI_TaxID=8410;
 (1)
 RN SEQUENCE FROM N.A.
 RX MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of
 z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008463; BAA36513.1; -;
 DR EMBL: AB008456; BAA36506.1; -;
 DR EMBL: AB008461; BAA36511.1; -;
 DR EMBL: AB008462; BAA36512.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 DR Membrane: Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;
 SQ
 Query Match 91.3%; Score 1409; DB 13; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1,9e-119;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEQAIISPAKDFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQYKGYIYDCYR 60
 DB 1 MTDVAISPAKDFLAGGVAIAISTAVAPIERVKLLQVQHSKQIADKQYKGYIYDCYR 60
 QY 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 DB 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 QY 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 DB 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDLGCLVTKSGDRIGLYQGFNS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDLGCLVTKSGDRIGLYQGFNS 180
 QY 181 VOGIITRAAYFEGVDYDAGMLDPKNTHTIVSMIAQVTVAAGVSYPPDVTYRRMM 240
 DB 181 VOGIITRAAYFEGVDYDAGMLDPKNTHTIVSMIAQVTVAAGVSYPPDVTYRRMM 240
 QY 241 OSGRKGADEIMYSGTIDCWKRIARDEGSRAPFGKAMSVNLGKGAFVLYLYDELKYYI 298
 DB 241 OSGRKGADEIMYSGTIDCWKRIARDEGSRAPFGKAMSVNLGKGAFVLYLYDELKYYI 298
 RESULT 8
 QYPRH2 PRELIMINARY; PRT: 298 AA.
 AC 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2003 (TREMblrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Winkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN SEQUENCE FROM N.A.
 RX MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of
 z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008460; BAA36510.1; -;
 DR EMBL: AB008458; BAA36508.1; -;
 DR EMBL: AB008459; BAA36509.1; -;

DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 DR Membrane: Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33062 MW; B0E225E67599A06 CRC64;
 SQ
 Query Match 91.1%; Score 1406; DB 13; Length 298;
 Best Local Similarity 88.3%; Pred. No. 3.6e-119;
 Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEQAIISPAKDFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQYKGYIYDCYR 60
 DB 1 MTDVAISPAKDFLAGGVAIAISTAVAPIERVKLLQVQHSKQIADKQYKGYIYDCYR 60
 QY 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 DB 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 QY 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 DB 61 IPKEGCVLSFWRGNLANVIRFPFOALNFAFKOKYKQIFLGGVDKHTQFMRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDLGCLVTKSGDRIGLYQGFNS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDLGCLVTKSGDRIGLYQGFNS 180
 QY 181 VOGIITRAAYFEGVDYDAGMLDPKNTHTIVSMIAQVTVAAGVSYPPDVTYRRMM 240
 DB 181 VOGIITRAAYFEGVDYDAGMLDPKNTHTIVSMIAQVTVAAGVSYPPDVTYRRMM 240
 QY 241 OSGRKGADEIMYSGTIDCWKRIARDEGSRAPFGKAMSVNLGKGAFVLYLYDELKYYI 298
 DB 241 OSGRKGADEIMYSGTIDCWKRIARDEGSRAPFGKAMSVNLGKGAFVLYLYDELKYYI 298
 RESULT 9
 QYPRH2 PRELIMINARY; PRT: 298 AA.
 AC 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-2003 (TREMblrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Winkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN SEQUENCE FROM N.A.
 RX MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of
 z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BAA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 DR Membrane: Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
 SQ
 Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 8.3e-119;
 Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEQAIISPAKDFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQYKGYIYDCYR 60
 DB 1 MTDVAISPAKDFLAGGVAIAISTAVAPIERVKLLQVQHSKQIADKQYKGYIYDCYR 60


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Dh 1 MTDAAISFAKDFLAGGAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKIMDCVVR 60
Qy 61 IPKEGCVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRRYFAGNLASG 120
Dh 61 IPKEGCVLSFWKGNLANVIRYPTQALNFAFKDKYKIFLDNDKRTQFWRRYFAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVYITKSDGIRGLYOGFSVS 180
Dh 121 GAAGATSLCFVYPLDFAKRLADVKGAGADREFKIGDCLAKIFRSDDGKGLYOGFSVS 180
Qy 181 VOGIIIRAAVFGVYPTAKGMLDPKNTHTIVSMMIAQVTVAVAGVSYFPDVRRRMM 240
Dh 181 VOGIIIRAAVFGVYPTAKGMLDPKNTHTIFISMMIAQSTVAVAGFASVYFPDVRRRMM 240
Qy 241 QSGRKADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298
Dh 241 QSGRKAEIMYSTIDCKMKIADDEGSRAPFKGAMSVNLKMGCAFVLVLYDELKRYI 298

RESULT 10
Q95VX4 PRELIMINARY; PRT; 299 AA.
ID 095VX4;
AC 095VX4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ADP-ATP translocator.
OS Ethmostigmus rubripes.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX NCBI_TaxID=62613;
RN [1]
RP SEQUENCE FROM N.A.
RA Burnell J.N.;
RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT rubripes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF01158; AAL02100.1;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR Pfam: PF00153; mlt_carri; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCARRIER.
SQ SEQUENCE. 299 AA; 33037 MW; 3C3B8CB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;
Best Local Similarity 81.5%; Pred. No. 1.5e-109;
Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MTEQAISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADKQYKGIIDCTVR 60
Dh 1 MTDAAISFAKDFLAGGAAAIKSTAVAPIERVKLLQVOHASKQIADKQYKGVDFEVR 60
Qy 61 IPKEGCVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRRYFAGNLASG 120
Dh 61 IPKEGCVLSFWKGNLANVIRYPTQALNFAFKDKYKIFLDNDKRTQFWRRYFAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVYITKSDGIRGLYOGFSVS 180
Dh 121 GAAGATSLCFVYPLDFAKRLADVKGAGADREFKIGDCLAKIFRSDDGKGLYOGFSVS 180
Qy 181 VOGIIIRAAVFGVYPTAKGMLDPKNTHTIVSMMIAQVTVAVAGVSYFPDVRRRMM 240
Dh 181 VOGIIIRAAVFGVYPTAKGMLDPKNTHTIFISMMIAQSTVAVAGFASVYFPDVRRRMM 240
Qy 241 QSGRKADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298
Dh 241 QSGRKADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 298

RESULT 11
Q91336 PRELIMINARY; PRT; 317 AA.
ID Q91336
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AC Q91336;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana sylvatica (Wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranolidae; Rana;
OX NCBI_TaxID=45438;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Liver;
RC TISSUE=Liver;
RX MEDLINE=97398141; Pubmed=9256066;
RA Cai Q., Greenway S.C., Storey K.B.;
RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
RT in wood frogs under freezing stress."
RL Biochim. Biophys. Acta 1353:69-78(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cai Q., Storey K.B.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: U44833; AAA97882.2;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR Pfam: PF00153; mlt_carri; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCARRIER.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 317 AA; 35005 MW; 5F6657ED8D5CEB72 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
Best Local Similarity 86.8%; Pred. No. 8.2e-106;
Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTEQAISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADKQYKGIIDCTVR 60
Dh 1 MTDAAISFAKDFLAGGAAAIKSTAVAPIERVKLLQVOHASKQIADKQYKIMDCVVR 60
Qy 61 IPKEGCVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRRYFAGNLASG 120
Dh 61 IPKEGCVLSFWKGNLANVIRYPTQALNFAFKDKYKIFLDNDKRTQFWRRYFAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVYITKSDGIRGLYOGFSVS 180
Dh 121 GAAGATSLCFVYPLDFAKRLADVKGAGADREFKIGDCLAKIFRSDDGKGLYOGFSVS 180
Qy 181 VOGIIIRAAVFGVYPTAKGMLDPKNTHTIVSMMIAQVTVAVAGVSYFPDVRRRMM 240
Dh 181 VOGIIIRAAVFGVYPTAKGMLDPKNTHTIFISMMIAQSTVAVAGFASVYFPDVRRRMM 240
Qy 241 QSGRKADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGCAFVLVLYDELKRYI 272
Dh 241 QSGRKAEIMYSTIDCKMKIADDEGSRAPFKGAMSVNLKMGCAFVLVLYDELKRYI 272

RESULT 12
Q81RAO PRELIMINARY; PRT; 312 AA.
ID Q81RAO;
AC Q81RAO;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CG16944-PC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe N.R., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abrell J.F., Abmayant A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Kapren G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li U., Li B., Lindsay L., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.E., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler M.P., Shih T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spiedling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhu Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Celinker S.E., Adams M.D., Krommler B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amandides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J.A., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K.J., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,
 RA Ferrieres S., Flise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Pacled J., Paragas V., Part S., Patel S., Pfeiffer B., Scheeler F.,
 RA Phouanavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Sytkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochank S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Clump M., Drysdale R., Emmert D., Flise E., de Grey A., Harris N.,
 RA Krommler B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.

RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003484; AAN09267.1; -
 SQ SEQUENCE 312 AA: 34214 MW: 7805634E74E168DF CRC64;
 Query Match 81.3%; Score 1254.5; DB 5; Length 312;
 Best Local Similarity 80.6%; Pred No 2,1e-105;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 QY 5 AISPANDFLAGIAAISKTVAPTEIEVKLLLOVQASQIADKQVGYDVCIRIPKE 64
 DB 20 AVEFVDFDFAAGISAAVSKTAVTEIEVKLLLOVQASQIADKQVGYDVCIRIPKE 79
 QY 65 QGVLSFWRGNLANVIRYPTQALNFAFKDKYKOITLGYDKTQWRIFAGNLAGGAG 124
 DB 80 QGVLSFWRGNLANVIRYPTQALNFAFKDKYKOITLGYDKTQWRIFAGNLAGGAG 139
 QY 125 ATSCFEYYPIDFARTRLAADYKSGTEREFGDCLVITKTSDSIGRLYOGFSVYOGI 184
 DB 140 ATSCFEYYPIDFARTRLAADYKSGTEREFGDCLVITKTSDSIGRLYOGFSVYOGI 198
 QY 185 IITPAAYFGYDPAKGLPDPKNTIIVSMIAQTYTAAVAVSVPTFVRRMMOSGR 244
 DB 199 IITPAAYFGYDPAKGLPDPKNTIIVSMIAQTYTAAVAVSVPTFVRRMMOSGR 258
 QY 245 KGADIMYTGVDCKRIFDEGKAFKGAISNVLKMGAFVLVYDELKKVI 298
 DB 259 KATVITKNTLHQMATIAQEGTGAFFKGAISNVLKMGAFVLVYDELKKVI 312
 RESULT 13
 Q9NHW5 PRELIMINARY; PRT; 300 AA.
 ID Q9NHW5
 AC Q9NHW5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Fteygota.
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilla.
 NX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF218587; AAF32322.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mlt_carrier.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCARRIER.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 300 AA: 33036 MW: 5459DF0EAD0E2E742 CRC64;
 Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5%; Pred No 1e-103;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;
 QY 6 ISFAPKDLAGIAAISKTVAPTEIEVKLLLOVQASQIADKQVGYDVCIRIPKE 65
 DB 9 LGEFVDFDFAAGISAAVSKTAVTEIEVKLLLOVQASQIADKQVGYDVCIRIPKE 68
 QY 66 GVLISFWRGNLANVIRYPTQALNFAFKDKYKOITLGYDKTQWRIFAGNLAGGAG 125
 DB 69 GVLISFWRGNLANVIRYPTQALNFAFKDKYKOITLGYDKTQWRIFAGNLAGGAG 128
 QY 126 TSICFEYYPIDFARTRLAADYKSGTEREFGDCLVITKTSDSIGRLYOGFSVYOGI 185

Dd	129	TSLSFVVPDLPDAFRRLAADTGKG-QREFGTGLGNCLAFIKFSDDGLVGRGVSVOGI	187
Qy	186	IYRAAYGVDTATAGMLPDPKNTHIVYSMMIAQVTYNAGAVSYSPFDVRRRMMQSGK	245
Dd	188	IYRAAYGFDFDTAGMLPDPKNPTPLYISMALAAVVTTYAGIYVSPFDVRRRMMQSGK	247
Qy	246	GADIMTYGVDCWKRIFDEGGAKFFFGAMSNNVLRGMGAPLVLYDELKKVI	298
Dd	248	ATEIIYKNTLHCMAITIAKOBTGAFFFGAFSNVLGTGAFVLYLDLKFL	300
RESULT 14			
ID	044093	PRELIMINARY;	PRT; 288 AA.
AC	044093;		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DN	ADP/ANP translocase (Fragment).		
GN	SesB.		
OS	Drosophila pseudoobscura (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
CC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
CC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_Taxid=7237;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;		
RL	Genetica 0:0-0(1997).		
CC	-1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
DR	EMBL: AF025786; AAB87883.1; -		
DR	FlyBase; FBgn003292; dpse\sesB.		
DR	InterPro; IPR001993; Mitochondrion_carrier.		
DR	InterPro; IPR002067; Mito_carrier.		
DR	Pfam; PF00153; mito_carr; 3.		
DR	PRINTS; PRO0926; MITOCARRIER.		
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.		
KM	Membrane; Repeat; Transmembrane; Transport.		
FT	NON_TER	288	
SO	SEQUENCE	288 AA; 31725 MW; 052BOCC0050436B0 CRC64;	
Query Match 77.0%; Score 1187.5; DB 5; Length 288; Best Local Similarity 80.7%; Pred. No.2.2e-99; Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3			
Qy	5	AISPAKDFLAGIAAISKTVAPIERYKLIIQYOHAASKQIADKQKGYDVCIARIPE	64
Dd	7	AIGVTKDPAAGISAASKTAVAPIERKLLIQYHISKQISPDKQKGMVDCFIRIRE	66
Qy	65	QGVLSPWRGNLANVIRFPOTALNFADFCKYKQJFLGVGVKHTQTFWRYPAGNLASGAAG	124
Dd	67	QGSSFWRCNLANVIRFPOTALNFAFKDYKQVFLGVDKNTQPFWRYFMNLASGAAG	126
Qy	125	ATSLCFVPLDPAFTRLAADVGKSTSEKEFNGLGSCYLKITMSDSIRGLYGQSFVSVOGI	184
Dd	127	ATSLCFVPLDPAFTRLAADVGKGS-QREFYGLGNCLRKIRFSDSLVGLYRFEVSVOGI	185
Qy	185	IYYAAAYGVVDTAAGMLPDPKNTHIVYSMMIAQTVTYNAGAVSYSPFDVRRRMMQSGR	244
Dd	186	IYYAAAYGVVDTAAGMLPDPKNTHIVYSMMIAQTVTYNAGAVSYSPFDVRRRMMQSGR	244
Qy	245	KGADIMTYGVDCWKRIFDEGGAKFFFGAMSNNVLRGMGAPLVLYDELKKVI	289
Dd	245	KATELIYKNTLHCMAITIAKOBETGAFFFGAFSNVLGTGAFVLYLDLKFL	288
RESULT 15			
ID	044094	PRELIMINARY;	PRT; 288 AA.
AC	044094;		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	

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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:10:07 ; Search time 29 Seconds

(without alignments)
434.781 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQALSPKADFLAGGIAAA.....LRMGCAFVLYLDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/Backfile01.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	4	US-09-434-354-49 Sequence 49, Appl
2	1454	94.2	298	4	US-09-434-354-48 Sequence 48, Appl
3	1412	91.5	298	3	US-08-961-871-10 Sequence 10, Appl
4	1385.5	89.8	297	4	US-09-434-354-47 Sequence 47, Appl
5	314	20.3	469	4	US-09-996-243-289 Sequence 289, App
6	311	20.2	469	3	US-09-188-930-339 Sequence 339, App
7	311	20.2	469	4	US-09-312-283C-339 Sequence 339, App
8	286	18.5	335	4	US-09-482-273-118 Sequence 118, App
9	283.5	18.4	291	4	US-09-501-558-2 Sequence 2, Appl
10	280	18.1	447	4	US-09-160-119-4 Sequence 4, Appl
11	280	18.1	674	4	US-09-160-119-2 Sequence 2, Appl
12	265	17.2	312	3	US-09-142-565-2 Sequence 2, Appl
13	250.5	16.2	299	1	US-08-518-878B-56 Sequence 56, Appl
14	250.5	16.2	299	1	US-08-470-868A-55 Sequence 55, Appl
15	250.5	16.2	309	1	US-08-518-878B-51 Sequence 51, Appl
16	250.5	16.2	309	2	US-08-807-861A-51 Sequence 51, Appl
17	250.5	16.2	309	2	US-08-470-868A-51 Sequence 51, Appl
18	250.5	16.2	309	3	US-09-210-681-51 Sequence 51, Appl
19	250.5	16.2	309	3	US-08-946-719A-51 Sequence 51, Appl
20	250.5	16.2	309	4	US-09-547-983-51 Sequence 51, Appl
21	250.5	16.2	311	2	US-08-775-009-33 Sequence 33, Appl
22	245	15.9	432	2	US-08-937-466-4 Sequence 4, Appl
23	245	15.9	432	2	US-09-172-528-4 Sequence 4, Appl
24	245	15.9	432	3	US-09-318-199-4 Sequence 4, Appl
25	245	15.9	432	3	US-09-503-579-4 Sequence 4, Appl
26	244	15.8	308	2	US-08-937-466-2 Sequence 2, Appl
27	244	15.8	308	2	US-09-172-528-2 Sequence 2, Appl

28	244	15.8	308	3	US-09-318-199-2	Sequence 2, Appl
29	244	15.8	308	3	US-09-503-579-2	Sequence 2, Appl
30	243.5	15.8	311	2	US-08-775-009-32	Sequence 32, Appl
31	232.5	15.1	320	2	US-08-933-750C-12	Sequence 12, Appl
32	232.5	15.1	320	3	US-09-234-613-12	Sequence 12, Appl
33	227.5	14.7	303	1	US-08-294-522B-36	Sequence 36, Appl
34	226.5	14.7	303	1	US-08-518-878B-37	Sequence 37, Appl
35	226.5	14.7	303	2	US-08-807-861A-37	Sequence 37, Appl
36	226.5	14.7	303	2	US-08-470-868A-37	Sequence 37, Appl
37	226.5	14.7	303	3	US-09-210-681-37	Sequence 37, Appl
38	226.5	14.7	303	3	US-08-946-719A-37	Sequence 37, Appl
39	226.5	14.7	303	4	US-09-547-983-37	Sequence 37, Appl
40	222	14.4	293	4	US-09-501-558-4	Sequence 4, Appl
41	211	13.7	306	5	PCT-US94-09799-1	Sequence 1, Appl
42	205.5	13.3	307	2	US-08-807-861A-56	Sequence 56, Appl
43	205.5	13.3	307	3	US-09-210-681-56	Sequence 56, Appl
44	205.5	13.3	307	3	US-08-946-719A-56	Sequence 56, Appl
45	205.5	13.3	307	4	US-09-547-983-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1									
US-09-434-354-49									
Sequence 49, Application US/09434354									
Patent No. 6562563									
GENERAL INFORMATION:									
APPLICANT: Murphy, Anne N.									
APPLICANT: Clevenger, William									
APPLICANT: Wiley, Sandra Eileen									
APPLICANT: Andreyev, Alexander Y.									
APPLICANT: Frigeri, Luciano G.									
APPLICANT: Velicelbi, Gonul									
APPLICANT: Davis, Robert E.									
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING									
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR									
FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS									
CURRENT APPLICATION NUMBER: 660088.433									
CURRENT FILING DATE: 1999-11-03									
NUMBER OF SEQ ID NOS: 54									
SOFTWARE: FASTSEQ for Windows Version 3.0									
SEQ ID NO 49									
LENGTH: 298									
TYPE: PRT									
ORGANISM: Homo sapien									
US-09-434-354-49									
Query Match									
Best Local Similarity 100.0%; Score 1543; DB 4; Length 298;									
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MTEQALSPKADFLAGGIAAISTKTAAPPIERVKLLIQVHASQIADQYKIVCIYR	60						
DB	1	MTEQALSPKADFLAGGIAAISTKTAAPPIERVKLLIQVHASQIADQYKIVCIYR	60						
QY	61	IPKEQGVLSFWKRNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRWYFAGNIASG	120						
DB	61	IPKEQGVLSFWKRNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRWYFAGNIASG	120						
QY	121	GAAGATSLCFVYPLDFARFLADVGKSGTEREFGIGDCLVYTKSDGIRGLYOGFSVS	180						
DB	121	GAAGATSLCFVYPLDFARFLADVGKSGTEREFGIGDCLVYTKSDGIRGLYOGFSVS	180						
QY	181	VQGIIRYRAVFEVYDTAKGMLDPDKNTHTVYSWMIAQVTVAVAGVSTPFDVRRRMAM	240						
DB	181	VQGIIRYRAVFEVYDTAKGMLDPDKNTHTVYSWMIAQVTVAVAGVSTPFDVRRRMAM	240						
QY	241	QSGRKADIMYTGTVDCMKRIIFDEGSKAFKFKAMSNVLRMGCAFVLYLDELKVI	298						
DB	241	QSGRKADIMYTGTVDCMKRIIFDEGSKAFKFKAMSNVLRMGCAFVLYLDELKVI	298						

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RESULT 2
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleveger, William
; APPLICANT: Wile, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigel, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: 660088.433
; CURRENT FILING DATE: 1999-11-03
; CURRENT APPLICATION NUMBER: US/09/434,354
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo saplen
US-09-434-354-48

Query Match
Best Local Similarity 94.2%; Score 1454; DB 4; Length 298;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISEFADFLAGGIAAISKTAAPAPIERVKLLLOVHASKQIADKQKGYDVCIVR 60
DB 1 MTDALSPFADFLAGGIAAISKTAAPAPIERVKLLLOVHASKQIADKQKGYDVCIVR 60
QY 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFEYPLDFAFRTLADVKGSGTEREFGDGLDCLVTKTSKDSGIRGLYOGFSVS 180
DB 121 GAAGATSLCFEYPLDFAFRTLADVKGSGTEREFGDGLDCLVTKTSKDSGIRGLYOGFSVS 180
QY 181 VOGIIRAAVFGVYDTAKGMLPDKNTHIVSWMLAQTVAVAGVSYFEDTVARRRMM 240
DB 181 VOGIIRAAVFGVYDTAKGMLPDKNTHIVSWMLAQTVAVAGVSYFEDTVARRRMM 240
QY 241 OSGRGADIYTGTVDCMKRIKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELTKK 296
DB 241 OSGRGADIYTGTVDCMKRIKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELTKK 296

RESULT 3
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10

Query Match
Best Local Similarity 91.5%; Score 1412; DB 3; Length 298;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISEFADFLAGGIAAISKTAAPAPIERVKLLLOVHASKQIADKQKGYDVCIVR 60
DB 1 MTDALSPFADFLAGGIAAISKTAAPAPIERVKLLLOVHASKQIADKQKGYDVCIVR 60
QY 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFEYPLDFAFRTLADVKGSGTEREFGDGLDCLVTKTSKDSGIRGLYOGFSVS 180
DB 121 GAAGATSLCFEYPLDFAFRTLADVKGSGTEREFGDGLDCLVTKTSKDSGIRGLYOGFSVS 180
QY 181 VOGIIRAAVFGVYDTAKGMLPDKNTHIVSWMLAQTVAVAGVSYFEDTVARRRMM 240
DB 181 VOGIIRAAVFGVYDTAKGMLPDKNTHIVSWMLAQTVAVAGVSYFEDTVARRRMM 240
QY 241 OSGRGADIYTGTVDCMKRIKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELTKK 298
DB 241 OSGRGADIYTGTVDCMKRIKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELTKK 298

RESULT 4
US-09-434-354-47
; Sequence 47, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleveger, William
; APPLICANT: Wile, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigel, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: 660088.433
; CURRENT FILING DATE: 1999-11-03
; CURRENT APPLICATION NUMBER: US/09/434,354
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo saplen
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1	PRIOR FILING DATE: 1998-06-17
2	PRIOR APPLICATION NUMBER: 60/089599
3	PRIOR FILING DATE: 1998-06-17
4	PRIOR APPLICATION NUMBER: 60/089600
5	PRIOR FILING DATE: 1998-06-17
6	PRIOR APPLICATION NUMBER: 60/089653
7	PRIOR FILING DATE: 1998-06-17
8	PRIOR APPLICATION NUMBER: 60/089801
9	PRIOR FILING DATE: 1998-06-18
10	PRIOR APPLICATION NUMBER: 60/089907
11	PRIOR FILING DATE: 1998-06-18
12	PRIOR APPLICATION NUMBER: 60/089908
13	PRIOR FILING DATE: 1998-06-18
14	PRIOR APPLICATION NUMBER: 60/089947
15	PRIOR FILING DATE: 1998-06-19
16	PRIOR APPLICATION NUMBER: 60/089948
17	PRIOR FILING DATE: 1998-06-19
18	PRIOR APPLICATION NUMBER: 60/089952
19	PRIOR FILING DATE: 1998-06-19
20	PRIOR APPLICATION NUMBER: 60/090246
21	PRIOR FILING DATE: 1998-06-22
22	PRIOR APPLICATION NUMBER: 60/090252
23	PRIOR FILING DATE: 1998-06-22
24	PRIOR APPLICATION NUMBER: 60/090254
25	PRIOR FILING DATE: 1998-06-22
26	PRIOR APPLICATION NUMBER: 60/090349
27	PRIOR FILING DATE: 1998-06-23
28	PRIOR APPLICATION NUMBER: 60/090355
29	PRIOR FILING DATE: 1998-06-23
30	PRIOR APPLICATION NUMBER: 60/090429
31	PRIOR FILING DATE: 1998-06-24
32	PRIOR APPLICATION NUMBER: 60/090431
33	PRIOR FILING DATE: 1998-06-24
34	PRIOR APPLICATION NUMBER: 60/090435
35	PRIOR FILING DATE: 1998-06-24
36	PRIOR APPLICATION NUMBER: 60/090444
37	PRIOR FILING DATE: 1998-06-24
38	PRIOR APPLICATION NUMBER: 60/090445
39	PRIOR FILING DATE: 1998-06-24
40	PRIOR APPLICATION NUMBER: 60/090472
41	PRIOR FILING DATE: 1998-06-24
42	PRIOR APPLICATION NUMBER: 60/090535
43	PRIOR FILING DATE: 1998-06-24
44	PRIOR APPLICATION NUMBER: 60/090540
45	PRIOR FILING DATE: 1998-06-24
46	PRIOR APPLICATION NUMBER: 60/090542
47	PRIOR FILING DATE: 1998-06-24
48	PRIOR APPLICATION NUMBER: 60/090557
49	PRIOR FILING DATE: 1998-06-24
50	PRIOR APPLICATION NUMBER: 60/090676
51	PRIOR FILING DATE: 1998-06-25
52	PRIOR APPLICATION NUMBER: 60/090678
53	PRIOR FILING DATE: 1998-06-25
54	PRIOR APPLICATION NUMBER: 60/090690
55	PRIOR FILING DATE: 1998-06-25
56	PRIOR APPLICATION NUMBER: 60/090694
57	PRIOR FILING DATE: 1998-06-25
58	PRIOR APPLICATION NUMBER: 60/090695
59	PRIOR FILING DATE: 1998-06-25
60	PRIOR APPLICATION NUMBER: 60/090696
61	PRIOR FILING DATE: 1998-06-25
62	PRIOR APPLICATION NUMBER: 60/090862
63	PRIOR FILING DATE: 1998-06-26
64	PRIOR APPLICATION NUMBER: 60/090865
65	PRIOR FILING DATE: 1998-06-26
66	PRIOR APPLICATION NUMBER: 60/091366
67	PRIOR FILING DATE: 1998-07-01
68	PRIOR APPLICATION NUMBER: 60/091478
69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091544
71	PRIOR FILING DATE: 1998-07-01
72	PRIOR APPLICATION NUMBER: 60/091519
73	PRIOR FILING DATE: 1998-07-02

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Query Match	20.3%;	Score 314;	DB 4;	Length 469;
Best Local Similarity	30.1%;	Pred. No. 7.8e-27;		
Matches	89;	Conservative	115;	Indels 32;
		Mismatches	115;	Gaps 11.

[illegible]

```

RESULT 6
US-09-188-930-339
US-09-188-930-339
Patent 339, Application US/09188930A
? ? Patent No. 6150502
? ? GENERAL INFORMATION:
? ? APPLICANT: Watson, James D.
? ? APPLICANT: Strachan, Lorna
? ? APPLICANT: Steeman, Matthew
? ? APPLICANT: Orrust, Renee
? ? APPLICANT: Morrison, James Greg
? ? TITLE OF INVENTION: Compositions Isolated
? ? TITLE OF INVENTION: and Methods For Their
? ? FILE REFERENCE: 11000.1011C1
? ? CURRENT APPLICATION NUMBER: US/09/188.930A
? ? CURRENT FILING DATE: 1998-11-09
? ? NUMBER OF SEQ ID NOS: 348
? ? SOFTWARE: FastSeq for Windows Version 3.0
? ? SEQ ID NO: 339
? ? LENGTH: 469
? ? TYPE: PRT
? ? ORGANISM: Mouse
US-09-188-930-339

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[illegible]


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Db      297 STYPMVLTAKM--LRKGT---QYSGMLDCARILLAKESGVAFYGYIPNMLGITPYAG 351
QY      190 AFGVYDTAKGMLPDKNTHI-----VSSMIAQYTAVAG--VSTPEPTVRRR 237
      352 IDLAVYETL-----KNTWLGKAVANSADPGVFLVLLAGCTISSGGLASPLALVRRR 404
QY      238 MMQSGRKADIMYGTVCWKRIKIFDEGKAFKFGKAMSNVLKMGCAV--LVLYDELK 295
      405 MQQASIEGAPVYTMSSL--FKOILRTGEGAFGLYRGLADPNFMKVIIPAVSISYVYENLK 461

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RESULT 7
US-09-312-283C-339
Sequence 339, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-339

Query Match 20.2%; Score 311; DB 4; Length 469;
Best Local Similarity 29.4%; Pred. No. 1.7e-26;
Matches 88; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

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QY      10 KQFLAGIAAISKTAVPRIERYKLLQYOHASKOIADKQYKIVDCIYRIKREGVLS 69
      188 RHLVAGGAGAVSRCTAPLDRKVLMOY--HNSR-----SNNMCYCGFQMRREGAGS 241
Db
QY      70 FMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGAAGATSLC 129
      242 LKRGNGINYLKIAPEBAIKFMAVEQMKR--LVGSDQET--LRHRLVAGSLAGAIQS 296
Db
QY      130 FVYPLDFARBRLLADVGKSGTEREFRLDCLVKIKKSGIKRLYGFVSVOGIIYRA 189
      297 STYPMVLTAKM--LRKGT---QYSGMLDCARILLAKESGVAFYGYIPNMLGITPYAG 351
Db
QY      190 AFGVYDTAKGMLPDKNTHI-----VSSMIAQYTAVAG--VSTPEPTVRRR 237
      352 IDLAVYETL-----KNTWLGKAVANSADPGVFLVLLAGCTISSGGLASPLALVRRR 404
QY      238 MMQSGRKADIMYGTVCWKRIKIFDEGKAFKFGKAMSNVLKMGCAV--LVLYDELK 295
      405 MQQASIEGAPVYTMSSL--FKOILRTGEGAFGLYRGLADPNFMKVIIPAVSISYVYENLK 461

```

RESULT 8
US-09-482-273-118
Sequence 118, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921

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; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 118
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (335)
; OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-118

```

Query Match 18.5%; Score 286; DB 4; Length 335;
Best Local Similarity 29.0%; Pred. No. 6.9e-24;
Matches 87; Conservative 50; Mismatches 133; Indels 30; Gaps 8;

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QY      10 KQFLAGIAAISKTAVPRIERYKLLQYOHAS-----KOIADKQYKIVDCIYRIKPE 64
      51 KPPVYGGIASYAEFGTFPVDTLKTRLQYOGOSIDARFKEI-----KYRGFAALFRICKE 106
Db
QY      65 QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGAAG 124
      107 EGVLYSGIAPRLHQASVGTIKIGIYOSLKRFLVERLEDEP-----LLINMIGVSG 161
QY      125 ATSLCFVYPLDFARTIADLVGKSGTEREFRLGDCIYITSDGIRGLYGFVSVOGI 184
      162 VIISTIANPPLDVLIKIMQA-----QSGLFQSGMIGS--FIDLYOEGTRGLMRGVPTAORA 216
Db
QY      185 IYRAAYFGVYDTAK-----GMLPDKNTHIYSSMIAQYTAVAGVSYPEPTVRRR 238
      217 AIYVGELVYVYDTLKTLLHLSGMDTIITHEVSSP-----TGLAGATLSNPDVYKTRM 272
QY      239 MMQSGRKADIMYGTVCWKRIKIFDEGKAFKFGKAMSNVLKMGCAV--LVLYDELK 297
      273 MNQRAIVGHVDLYKGTVDGILKMKMKHEGFALYKGFWMPLRLGPNWIIFFIYEQDKRL 332
Db

```

RESULT 9
US-09-501-558-2
Sequence 2, Application US/09501558
Patent No. 6403784
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6403784e1 Human uncoupling Proteins and
FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-09-501-558-2

Query Match 18.4%; Score 283.5; DB 4; Length 291;
Best Local Similarity 28.9%; Pred. No. 1.1e-23;
Matches 87; Conservative 54; Mismatches 129; Indels 31; Gaps 9;

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QY      10 KQFLAGIAAISKTAVPRIERYKLLQYOHAS-----KOIADKQYKIVDCIYRIKPE 64
      7 KPPVYGGIASYAEFGTFPIDLKTRLQYOGOTNDKAFKEI-----KYRGFAALVIRIGRE 62
Db
QY      65 QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGAAG 124

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Db      63  EGIAMXSGIAPMAMQASVGIKIGTYOSLKRIFIRPDEI-----LPVIVIGILSG 117
Qy      125  ATSLCFYPIIDFARTLADVCKSGTEREFGIDCLVTKSGDJRGYOGESVYOGI 184
Db      118  VISSTIANFDVLRKMQA-----QSNITQ--GGMIGNFMNIYQOEGRGIMKGVSLFAQRA 172
Qy      165  IYRAAFYGYDTRK-----GMLDPKNTHTIVSMIAQTVTAAGVYVPEDFVRRRM 238
Db      173  AIVGVLEPYDITKHLISLGMGYITHTLSF-----TCLAGALASNPVDVYTRM 228
Qy      239  MMQSG-RKGDIMYTGVDCKMRIRDEGKAFFRGKAMSVLK-GMGAFVLYLDELK 296
Db      229  MNQRYLKDGRCSGYTGLDCLQITMKNRSGFALYKGFPMNLKGFPMNLIIFVYIEQLK 288
Qy      297  V 297
Db      289  L 289
```

```
RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEM, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRF
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
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Query Match      18.1%; Score 280; DB 4; Length 447;
Best Local Similarity 27.1%; Pred No. 5.1e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;
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Qy      4  QAIISAKDFLAGIAAISTATAPIERVKLLQVHASKQIADKQKGIYDCIVRIPK 63
Db      96  QVNESYRFGLSVAGAVATVYFDLVKTRMQRSTSGFVGLMTKNSFDCFKYLR 155
Qy      64  EGVLSFMRGNLANVIRYFTQALNFAFKDKYKQIFL---GGVDKHTQFMRFRAGNLASG 120
Db      156  YEFEGFLYRGLLPOLLGVAPKAKIKLVNDFVRDKFMHNDGSP-----LAAETILAG 207
Qy      121  GAAGATSLCFYPIIDFARTLADVCKSGTEREFGIDCLVTKSGDJRGYOGESVS 180
Db      208  GCAGGSOVYFTNPLEYKIRIQV-AGEITTPRVSL-----SVYRDGFFGGLYKAKAC 261
Qy      181  VOGIITIRAAVFGVYDTRAKMLDPRKNTHTIVSMIAQTVTA-AGVSYPPDFVRRRM 239
Db      262  FLMDIYFSATYPPCYAHAKASFANEDQVSPGSLLAGIAGMPAASIVTPADVIKTR-- 319
Qy      240  MOSGRGADIMYTGVDCKMRIRFDEGKAFFRGKAMSVLKMGAFVLYLDEL 294
Db      320  LQVAAAGQTYSSVIDCFRKLIREGPKALMKGAGARVERSSPOGVTLLTYEL 374
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEM, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRF
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
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Query Match      18.1%; Score 280; DB 4; Length 674;
Best Local Similarity 27.1%; Pred No. 9.4e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;
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Qy      4  QAIISAKDFLAGIAAISTATAPIERVKLLQVHASKQIADKQKGIYDCIVRIPK 63
Db      323  QVNESYRFGLSVAGAVATVYFDLVKTRMQRSTSGFVGLMTKNSFDCFKYLR 382
Qy      64  EGVLSFMRGNLANVIRYFTQALNFAFKDKYKQIFL---GGVDKHTQFMRFRAGNLASG 120
Db      383  YEFEGFLYRGLLPOLLGVAPKAKIKLVNDFVRDKFMHNDGSP-----LAAETILAG 434
Qy      121  GAAGATSLCFYPIIDFARTLADVCKSGTEREFGIDCLVTKSGDJRGYOGESVS 180
Db      435  GCAGGSOVYFTNPLEYKIRIQV-AGEITTPRVSL-----SVYRDGFFGGLYKAKAC 488
Qy      181  VOGIITIRAAVFGVYDTRAKMLDPRKNTHTIVSMIAQTVTA-AGVSYPPDFVRRRM 239
Db      489  FLMDIYFSATYPPCYAHAKASFANEDQVSPGSLLAGIAGMPAASIVTPADVIKTR-- 546
Qy      240  MOSGRGADIMYTGVDCKMRIRFDEGKAFFRGKAMSVLKMGAFVLYLDEL 294
Db      547  LQVAAAGQTYSSVIDCFRKLIREGPKALMKGAGARVERSSPOGVTLLTYEL 601
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RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Palme
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704511.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRF
; ORGANISM: HOMO SAPIEN
US-09-142-565-2
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Query Match      17.2%; Score 265; DB 3; Length 312;
Best Local Similarity 27.1%; Pred. No. 1.5e-21;
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:13:53 ; Search time 57 Seconds
(without alignments)
684.894 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEQAIISPAKDFLAGGIAAA.....LRMGCAFVLYLDEIKKYI 298

Scoring table: BIOSUM62
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1543	100.0	298	9 US-09-811-094-33	Sequence 33, Appl
2	1543	100.0	298	9 US-09-810-644-33	Sequence 33, Appl
3	1543	100.0	298	10 US-09-185-904A-33	Sequence 33, Appl
4	1454	94.2	298	9 US-09-811-094-32	Sequence 32, Appl
5	1454	94.2	298	10 US-09-810-644-32	Sequence 32, Appl
6	1454	94.2	298	10 US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.8	297	9 US-09-811-094-31	Sequence 31, Appl
8	1385.5	89.8	297	9 US-09-810-644-31	Sequence 31, Appl
9	1385.5	89.8	297	10 US-09-185-904A-31	Sequence 31, Appl
10	760.5	49.3	318	10 US-09-801-368-252	Sequence 252, Appl
11	749.5	48.6	366	9 US-09-734-569-170	Sequence 170, Appl
12	737	47.8	308	15 US-10-128-714-3338	Sequence 3338, Appl
13	737	47.8	308	15 US-10-128-714-8338	Sequence 8338, Appl
14	734.5	47.6	381	12 US-10-141-478A-2	Sequence 192, Appl
15	686	44.5	677	12 US-10-259-165-192	

16	518	33.6	132	9 US-09-925-301-1459	Sequence 1459, Appl
17	423	27.4	87	9 US-09-864-761-36440	Sequence 36440, A
18	368	23.8	475	10 US-09-777-921A-4	Sequence 4, Appl1
19	368	23.8	477	10 US-09-777-921A-2	Sequence 2, Appl1
20	333.5	21.6	410	10 US-09-777-921A-5	Sequence 5, Appl1
21	314	20.3	469	9 US-09-989-722-289	Sequence 289, Appl
22	314	20.3	469	9 US-09-989-723-289	Sequence 289, Appl
23	314	20.3	469	9 US-09-989-729-289	Sequence 289, Appl
24	314	20.3	469	9 US-09-989-727-289	Sequence 289, Appl
25	314	20.3	469	10 US-09-989-731-289	Sequence 289, Appl
26	314	20.3	469	10 US-09-989-732-289	Sequence 289, Appl
27	314	20.3	469	10 US-09-991-073-289	Sequence 289, Appl
28	314	20.3	469	10 US-09-990-442-289	Sequence 289, Appl
29	314	20.3	469	10 US-09-993-163-289	Sequence 289, Appl
30	314	20.3	469	10 US-09-993-604-289	Sequence 289, Appl
31	314	20.3	469	10 US-09-990-456-289	Sequence 289, Appl
32	314	20.3	469	10 US-09-989-721-289	Sequence 289, Appl
33	314	20.3	469	10 US-09-992-598-289	Sequence 289, Appl
34	314	20.3	469	10 US-09-989-293A-289	Sequence 289, Appl
35	314	20.3	469	10 US-09-989-735-289	Sequence 289, Appl
36	314	20.3	469	10 US-09-990-444-289	Sequence 289, Appl
37	314	20.3	469	10 US-09-991-181-289	Sequence 289, Appl
38	314	20.3	469	10 US-09-989-730-289	Sequence 289, Appl
39	314	20.3	469	10 US-09-990-436-289	Sequence 289, Appl
40	314	20.3	469	10 US-09-993-687-289	Sequence 289, Appl
41	314	20.3	469	11 US-09-989-734-289	Sequence 289, Appl
42	314	20.3	469	11 US-09-997-653-289	Sequence 289, Appl
43	314	20.3	469	11 US-09-993-667-289	Sequence 289, Appl
44	314	20.3	469	11 US-09-997-428-289	Sequence 289, Appl
45	314	20.3	469	11 US-09-997-666-289	Sequence 289, Appl

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Waller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AMT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811.094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRN
ORGANISM: Homo sapien
US-09-811-094-33
Query Match 100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 66-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAIISPAKDFLAGGIAAISTYAVAPIERVALLQVHASKQIAADKQKGIYDCTVR 60
DB 1 MTEQAIISPAKDFLAGGIAAISTYAVAPIERVALLQVHASKQIAADKQKGIYDCTVR 60
QY 61 IPKEQGLSWRGNLANVIRYPTQALNFKFKKRYKQIFLGVDKHTQFRYRAGNIASG 120
DB 61 IPKEQGLSWRGNLANVIRYPTQALNFKFKKRYKQIFLGVDKHTQFRYRAGNIASG 120

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Page 2

OY 121 GAAGATSLCFVYPLDFAFTRILADVGSKTEREFGIGDCLVYKISDGINGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFAFTRILADVGSKTEREFGIGDCLVYKISDGINGLYOGFSVS 180
OY 181 VOGIITIRAAVFGVYDTAKGMLDPKKNTHIVVSMIAQVTAAGVAVSYPEFVRRMM 240
DB 181 VOGIITIRAAVFGVYDTAKGMLDPKKNTHIVVSMIAQVTAAGVAVSYPEFVRRMM 240
OY 241 OSGRKADIMYTGTCVCKMKIRFDEGKAFKFGAMS NVLKGMGAFVLVYDELKKVI 298
DB 241 OSGRKADIMYTGTCVCKMKIRFDEGKAFKFGAMS NVLKGMGAFVLVYDELKKVI 298

RESULT 2

US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D3
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRF
ORGANISM: Homo sapien
US-09-810-644-33

Query Match 100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQATSFADFLAGGIAAISTKTA VAPIERVKLLQVOHASKOIAADKQYGI VDCIYR 60
DB 1 MTEQATSFADFLAGGIAAISTKTA VAPIERVKLLQVOHASKOIAADKQYGI VDCIYR 60
OY 61 IPKOGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMWYFAGNLASG 120
DB 61 IPKOGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMWYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFAFTRILADVGSKTEREFGIGDCLVYKISDGINGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFAFTRILADVGSKTEREFGIGDCLVYKISDGINGLYOGFSVS 180
OY 181 VOGIITIRAAVFGVYDTAKGMLDPKKNTHIVVSMIAQVTAAGVAVSYPEFVRRMM 240
DB 181 VOGIITIRAAVFGVYDTAKGMLDPKKNTHIVVSMIAQVTAAGVAVSYPEFVRRMM 240
OY 241 OSGRKADIMYTGTCVCKMKIRFDEGKAFKFGAMS NVLKGMGAFVLVYDELKKVI 298
DB 241 OSGRKADIMYTGTCVCKMKIRFDEGKAFKFGAMS NVLKGMGAFVLVYDELKKVI 298

RESULT 3

US-09-185-904A-33
Sequence 33, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.

APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRF
ORGANISM: Homo sapien
US-09-185-904A-33

Query Match 100.0%; Score 1543; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQATSFADFLAGGIAAISTKTA VAPIERVKLLQVOHASKOIAADKQYGI VDCIYR 60
DB 1 MTEQATSFADFLAGGIAAISTKTA VAPIERVKLLQVOHASKOIAADKQYGI VDCIYR 60
OY 61 IPKOGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMWYFAGNLASG 120
DB 61 IPKOGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMWYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFAFTRILADVGSKTEREFGIGDCLVYKISDGINGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFAFTRILADVGSKTEREFGIGDCLVYKISDGINGLYOGFSVS 180
OY 181 VOGIITIRAAVFGVYDTAKGMLDPKKNTHIVVSMIAQVTAAGVAVSYPEFVRRMM 240
DB 181 VOGIITIRAAVFGVYDTAKGMLDPKKNTHIVVSMIAQVTAAGVAVSYPEFVRRMM 240
OY 241 OSGRKADIMYTGTCVCKMKIRFDEGKAFKFGAMS NVLKGMGAFVLVYDELKKVI 298
DB 241 OSGRKADIMYTGTCVCKMKIRFDEGKAFKFGAMS NVLKGMGAFVLVYDELKKVI 298

RESULT 4

US-09-811-094-32
Sequence 32, Application US/09811094
Patent No. US2001004414A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRF
ORGANISM: Homo sapien
US-09-811-094-32

Query Match 94.2%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 2e-147;

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Page 4

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-811-094-31

Query Match
Best Local Similarity 89.8%; Score 1385.5; DB 9; Length 297;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSPADFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
1 MGDHAWSEFLKDFLAGAATAVAVSTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
DB 1 MTEQALSPADFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
QY 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 180
121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 180
DB 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 179
QY 181 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 240
180 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 239
DB 180 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 239
QY 241 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 298
240 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 297
DB 240 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 297

RESULT 8
US-09-810-644-31
; Sequence 31, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moser, Walter H.
; APPLICANT: Fel, Izabong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810.644
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-810-644-31

Query Match
Best Local Similarity 89.8%; Score 1385.5; DB 9; Length 297;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
QY 1 MTEQALSPADFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
1 MGDHAWSEFLKDFLAGAATAVAVSTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
DB 1 MTEQALSPADFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
QY 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 180
121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 180
DB 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 179

DB 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 179
QY 181 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 240
180 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 239
DB 180 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 239
QY 241 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 298
240 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 297
DB 240 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 297

RESULT 9
US-09-185-904A-31
; Sequence 31, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185.904A
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-185-904A-31

Query Match
Best Local Similarity 89.8%; Score 1385.5; DB 10; Length 297;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
QY 1 MTEQALSPADFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
1 MGDHAWSEFLKDFLAGAATAVAVSTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
DB 1 MTEQALSPADFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKIVDCIVR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOPMRYFAGNLASG 120
QY 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 180
121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 179
DB 121 GAAGTSLCFYPLDFAKRLADVGRR-AQREFHGLGDCIIRKFSDDLRLGLYGFNVS 179
QY 181 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 240
180 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 239
DB 180 VGGIITRAAFVGYDPAKMLDPKRNHIYVSMIAQTYAAGVSYPTDVRRRMM 239
QY 241 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 298
240 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 297
DB 240 QSGRKGADIMYTGVDCKRIKIFDEGKAFKAGANSVLRMGAGFVLYLDELKVI 297

RESULT 10
US-09-801-368-252
; Sequence 252, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary

? APPLICANT: Milne, Todd
 ? APPLICANT: No. US20020128250A1man, Thea
 ? APPLICANT: Royer, John
 ? APPLICANT: Salama, Sofie
 ? APPLICANT: Sherman, Amir
 ? APPLICANT: Silva, Jeff
 ? APPLICANT: Summers, Eric
 ? TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungl
 ? FILE REFERENCE: 109272.147
 ? CURRENT APPLICATION NUMBER: US/09/801,368
 ? PRIORITY FILING DATE: 2001-03-07
 ? PRIOR APPLICATION NUMBER: US 09/487,558
 ? PRIOR FILING DATE: 2000-01-19
 ? PRIOR APPLICATION NUMBER: US 60/160,587
 ? PRIOR FILING DATE: 1999-10-20
 ? NUMBER OF SEQ ID NOS: 440
 ? SOFTWARE: PatentIn version 3.0
 ? SEQ ID NO 252
 ? LENGTH: 318
 ? TYPE: PRF
 ? ORGANISM: *Saccharomyces cerevisiae*
 ? US-09-801-368--252

Query Match	Score	DB	Length
49.38;	760.5;	10;	318;

Best Local Similarity 53.7%; Pred. No. 4.4e-73;
Matches 159; Conservative 42; Mismatches 86; Indels 9; Gaps 5

QY 7 7SEAKDFLGGIAAIAISKTAAPLPIERVKLLQVQ-HASKRIADSDQKGYADCVIAPKEQ 65
 22 NFILDFLGGVSAVAKTAASPIERVKLLIQNDQEMLKQGLDKRYAGIILDCFKTATQ 81

QY 66 GYLSFWRNLTANYIRYEPFOALNDFKDKYKQILGLGVDRKHTGEWRFFGNLASGAAGA 125
 82 GYLSFWRNLTANYIRYEPFOALNDFKDKYKQILGLGVDRKHTGEWRFFGNLASGAAGA 139

OY 126 TSLCFVRYLDFARTRLAD - VGSSTGEREFRGDCLYKTKTSGRIGELYGFESVSVOG 183
| | | | | | | | | | : | | | | |
Db 140 LSLFVYSLDYARTRLADSKSSKKGGAOFNGIDVRYKTLKSQVAGVIRGFLEPSVVG 199
| | | | | | | | | | : | | | | |

OY 184 IITRYRAAFGVYDTAKG--MLPDKRNTHTIVSWMTAQTYAVAGVSYPEPTVRRMMMS 242
:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Nb 200 IVYRGLEFGMYSLKPLLTGTSGEASFASFLIGMNVYTGAISCSYPIEDTVRRMMTS 259
:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

QY 243 GRRGADIMTGTATDCWKRIFRDEGGKAPFFKGAMSNVLRGMGAPLVLYDELKAYI 298
b 260 GGA--VYDDGAPDCLRKIVAAEEVSGSEFGCGNNILFRVAGAGVASYMDLOMLI 312

RESULT 11
US-09-734-569-170

```

Sequence 170, Application US/09734569
Patent No. US20020064816A1
GENERAL INFORMATION:
APPLICANT: Derschl, Jens
APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
APPLICANT: Reinold, Andreas
APPLICANT: Cirus, Petra
APPLICANT: Bischoff, Friedrich
APPLICANT: Frank, Markus
APPLICANT: Freund, Annette
APPLICANT: Duvenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Reski, Ralf
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
in the synthesis of carbohydrates
FILE REFERENCE: BASF-NAE-1332-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIORITY APPLICATION NUMBER: US 60/171,101
PRIORITY FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1

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; SEQ ID NO 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-170

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Query Match 48.6%; Score 749.5; DB 9; Length 386;

Best Local Similarity 53.4%; Pred. No. 8.6e-72;
Matches 157; Conservative 44; Mismatches 84; Indels 9; Gaps 5

Db	75	SEAKDFLAGGIAAISKTAAPIERVKLLQV-HASKOIAADKQYKGIVDCIVIRPEKQ	65
Qy	84	SEMTDFLNGGSAVAASKTAAPIERVKLLIQNDMLKSGRLSHDKYGIECFSTVKVD	143

OY 66GVSIFWRGLTANYTRYFPFOALNAFCKDYKQIFGVGNKHTEFRYPASNLASGAAGA 125
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 144 GMSLWRRGTANTAYTRYFPFOALNAFKDKFYSLSEYGKKRK - DGYSWKPFANLASGAAGA 202

Oy 126TSCFVYPLDEAFRTADLVY---GKSGTEEFRRGDCLVKITKSQDGRILEYQGSSVSQ 182
Db 203SSLFFVYSLSLDYARTRLANDAKSSRKGGEGEQFNGLVDVYKKTLTDGIABLYRGFAISCA 262

Oy 183 GIIIRAAVEGYDTAKG-MLPDKRNTHTLVSNMIAQTYAVAGVSYSPEDTVRRRMMQ 241
 Db 263 GIIIRKGIYFGIDSLKPVVLGNLEGNELASFLGWMGITIGAGIASLPIDTVRRMMT 322

QY 242 SGRKGADIMYTGIVDCWKRIIFRDEGSKAFPFKGAANSVNLKRMGGAIVLVLYDELK 295

Db 333 SGEE--KYNGSDPAFKOILAKEGAKSLFEGAGANILIRVAVAGAVLSGVDO 373

RESULT 12
US-10-128-714-3338

; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jland, Bo

```

;
;
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Froshtin, Aleksey M

```

AFFILIATION: Lemnua, seaduction M
 TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigata
 TITLE OF INVENTION: Methods of Use
 REFERENCE: 10182-018-000

CURRENT APPLICATION NUMBER: US 10/128,114
 CURRENT FILING DATE: 2002-04-23
 PRIOR APPLICATION NUMBER: US 60/285,697
 PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
FILING DATE: 2001-05-05

PRIOR APPLICATION NUMBER: US 60/303,899
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-03

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;
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3338

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; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3338

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Query Match	47.8%;	Score 737;	DB 15;	Length 308;
Best Local Similarity	51.7%;	Pred. No. 1.4e-70;		
Matches 154;	Conservative 47;	Mismatches 85;	Indels 12;	Gaps 6

Oy 7 SPKDFDLGGIAAISTKVAPIRVKLLQVCHASKOIA---DKQYKGIVDCIYRIPK 63
Db 7 AFITDSFAVGVSAAVSKTAAPIERIKLL--VNQDEMTIRAGRLDRKYNGIIDCERRTAQ 64

```
OY 64 EOGVLSFMRGNLANVIRFPTQALNFAFKDYKQIFLGVDKHTQFWRYFAGNLSGAA 123
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 AEGVMSLMRGNTANVIRFPTQALNFAFRDYKSKMFAVKDR-DGYAKMMGMNLSGAA 123
OY 124 GATSLCEFYPLDPFARTRLAADV--GKSGTEREERFGJGDCLVKTKYSDGIRGLYOGFSVY 181
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 GATSLCEFYPLDPFARTRLAADV--GKSGTEREERFGJGDCLVKTKYSDGIRGLYOGFSVY 183
OY 182 OGIIYRAAYGVYDVIKAG-MLPDPKNTHTIVSMMIAQVTYAVAGVSYEPDVRMM 240
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 LGIIVYRGILYCGMDSIKPVLVSGSLGSLASFLLGVTGTGAGIASYELDTIRRRMM 243
OY 241 OSGRKGADIMYTGVDCKRIKIFDEGKAFKFGAAMSVLRGMGAFLVLYDELKVI 298
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 TSGEA---VKYKSSLDAAKQIIAKEGVKSLFKGAGANILRGVAGVLSYDQVOLL 298

RESULT 13
US-10-128-714-8338
; Sequence 8338, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengli
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshekin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8338
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8338

Query Match 47.8%; Score 737; DB 15; Length 308;
Best Local Similarity 51.7%; Pred. No. 1,4e-70;
Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;

OY 7 SFADFLAGGIAAISKTAAPIERVKLLQVQHASKOIAA---DKOYGIYDCIYRIPK 63
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Db 7 AFDSDFAVGVSAVSKTAAPIERIKLL--VONDEMIKRGIRDRKNGIIDCFRRTAO 64
OY 64 EOGVLSFMRGNLANVIRFPTQALNFAFKDYKQIFLGVDKHTQFWRYFAGNLSGAA 123
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 AEGVMSLMRGNTANVIRFPTQALNFAFRDYKSKMFAVKDR-DGYAKMMGMNLSGAA 123
OY 124 GATSLCEFYPLDPFARTRLAADV--GKSGTEREERFGJGDCLVKTKYSDGIRGLYOGFSVY 181
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 GATSLCEFYPLDPFARTRLAADV--GKSGTEREERFGJGDCLVKTKYSDGIRGLYOGFSVY 183
OY 182 OGIIYRAAYGVYDVIKAG-MLPDPKNTHTIVSMMIAQVTYAVAGVSYEPDVRMM 240
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Db 184 LGIIVYRGILYCGMDSIKPVLVSGSLGSLASFLLGVTGTGAGIASYELDTIRRRMM 243
OY 241 OSGRKGADIMYTGVDCKRIKIFDEGKAFKFGAAMSVLRGMGAFLVLYDELKVI 298
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RESULT 14
US-10-141-478A-2
; Sequence 2, Application US/10141478A
; Publication No. US20030148300A1
; GENERAL INFORMATION:
; APPLICANT: Valentin, Henry
; APPLICANT: Savage, Thomas
; APPLICANT: Voelker, Toni
; APPLICANT: Zang, Wei
; TITLE OF INVENTION: Metabolite Transporters
; FILE REFERENCE: 16515.146
; CURRENT APPLICATION NUMBER: US/10/141,478A
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: US 60/289,519
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,527
; PRIOR FILING DATE: 2001-05-09
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1. 165
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-141-478A-2

Query Match 47.6%; Score 734.5; DB 12; Length 381;
Best Local Similarity 52.5%; Pred. No. 3,4e-70;
Matches 159; Conservative 44; Mismatches 79; Indels 21; Gaps 7;

OY 7 SFADFLAGGIAAISKTAAPIERVKLLQVQHASKOIAA---DKOYGIYDCIYRIPK 63
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Db 7 NFAFDPLMGVSAVSKTAAPIERVKLLIQN--DEMTAGRLSEPYGIDDCGRYIK 136
OY 64 EOGVLSFMRGNLANVIRFPTQALNFAFKDYKQIFLGVDKHTQFWRYFAGNLSGAA 123
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 DEGRSLMRGTANVIRFPTQALNFAFRDYKSKMFAVKDR-DGYAKMMGMNLSGAA 195
OY 124 GATSLCEFYPLDPFARTRLAADV--GKSGTEREERFGJGDCLVKTKYSDGIRGLYOGFSVY 180
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 GATSLCEFYPLDPFARTRLAADV--GKSGTEREERFGJGDCLVKTKYSDGIRGLYOGFSVY 255
OY 182 OGIIYRAAYGVYDVIKAG-MLPDPKNTHTIVSMMIAQVTYAVAGVSYEPDVRMM 240
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIYRAAYFGYDVIKAG-MLPDPKNTHTIVSMMIAQVTYAVAGVSYEPDVRMM 235
OY 236 RRMNMGSRKGADIMYTGVDCKRIKIFDEGKAFKFGAAMSVLRGMGAFLVLYDELK 295
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 312 RRMNMTSNEA---VKYKSSLDAAKQIIAKEGVKSLFKGAGANILRGVAGVLSYDQVOLL 368
OY 296 KVI 298
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Db 369 LTV 371

RESULT 15
US-10-259-165-192
; Sequence 192, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; APPLICANT: Chang, Hur-seong
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: Kreps, Joel
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; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 syngenta
; SEQ ID NO 192
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-192
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Query Match 44.5%; Score 686; DB 12; Length 677;

Best Local Similarity 50.3%; Pred. No. 1.2e-64;

Matches 155; Conservative 43; Mismatches 88; Indels 22; Gaps 9;

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QY      3 EOAIS-FAKDFLAGIAAIAISKTAVAPIERVKLLQVO-HASKQIAADKQYKGIYDCIVR 60
DB      370 EKGLSGFMDFFMGMGVSAAVSKTAAPTERIKLLIQNDEMITSGRLSHPYGIADCFGR 429
QY      61 IPKEGVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
DB      430 TKDEGVIALMRGNANVIRYFPQALNFAFKDHFRMFEFRKDK-DGYMKWFAGNLASG 488
QY      121 GAAGATSLCEVYPLDFARTRLAAD--VGKSGTEREPRGLDCLVKTITSGDGRGLY--Q 175
DB      489 GAAGACSLFVYSLDYARTRLANDAKAAKGGGRQPNGLVDYRKTLASDGIAGLTPWIQ 548
QY      176 GFSVSVGGIIYRAAYFGVYDTAK-----GMLPDPKNTIIVSWMIAQTVAAGVSYR 230
DB      549 HLPVLVS--LSNRGLYFGYDSLKPVLVGNLQD---NFLASFLGNGITIGAGLASYP 602
QY      231 PDTVRRRMNMGSRGADIMTGTCDCKRKIFRDEGGAFFFGAMSNTVLRGMGAFVLYL 290
DB      603 IDTVRRRMNMTSGEA--VKYNSLDAFRQIVAKGAKSLFRGAGANILRAVAGAGVLAG 659
QY      291 YDELKKVI 298
DB      660 YDKLQVV 667
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Job time : 59 secs

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